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OM protein - protein search, using sw model

Run on: May 10, 2003, 23:15:14 ; Search time 238 Seconds

(Without alignments)
67.994 Million cell updates/sec

Title: US-09-905-657-2

Perfect score: 2848
Sequence: 1 MGRSNEODLLSTELVNRGIF.....KKPTRRNPWVCINRYPVPL 550

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2845	99.9	550	4 US-08-868-373-8	Sequence 8, Appl
2	1569	55.1	516	4 US-08-868-373-14	Sequence 14, Appl
3	1493	52.4	537	4 US-08-868-373-10	Sequence 10, Appl
4	1446.5	50.8	500	4 US-08-868-373-12	Sequence 12, Appl
5	1445	50.7	497	4 US-09-058-947A-4	Sequence 4, Appl
6	1438	50.5	520	4 US-08-868-373-2	Sequence 2, Appl
7	1194	41.9	493	4 US-08-868-373-4	Sequence 4, Appl
8	1186	41.6	506	3 US-08-868-998-2	Sequence 2, Appl
9	1186	41.6	506	4 US-09-362-633-2	Sequence 2, Appl
10	1170.5	41.1	504	4 US-08-868-373-6	Sequence 6, Appl
11	334	11.7	127	3 US-08-868-998-4	Sequence 4, Appl
12	334	11.7	127	4 US-09-362-633-4	Sequence 4, Appl
13	169.5	6.0	349	4 US-08-994-035C-5	Sequence 5, Appl
14	169.5	6.0	349	4 US-09-395-861-5	Sequence 5, Appl
15	166.5	5.8	349	2 US-08-494-907-12	Sequence 12, Appl
16	166.5	5.8	349	5 PCT-US96-10986-12	Sequence 12, Appl
17	151.5	5.3	333	4 US-09-134-001C-3946	Sequence 3946, Ap
18	148.5	5.2	83	4 US-09-145-828A-2	Sequence 2, Appl
19	125.5	4.4	394	4 US-09-252-816A-1	Sequence 1, Appl
20	113	4.0	1094	2 US-08-680-326-40	Sequence 40, Appl
21	102	3.6	420	4 US-09-213-053-4	Sequence 4, Appl
22	102	3.6	1394	4 US-09-213-053-2	Sequence 2, Appl
23	97.5	3.4	324	1 US-08-746-797-2	Sequence 2, Appl
24	97.5	3.4	324	1 US-08-927-387-2	Sequence 2, Appl
25	97.5	3.4	324	2 US-08-918-058-2	Sequence 2, Appl
26	96.5	3.4	307	4 US-09-134-001C-5144	Sequence 5144, Ap
27	96	3.4	903	2 US-08-209-521-24	Sequence 24, Appl

28	96	3.4	903	4 US-08-961-810-134	Sequence 134, App
29	96	3.4	903	4 US-08-352-902D-134	Sequence 134, App
30	95.5	3.4	682	1 US-07-998-003A-107	Sequence 107, App
31	95.5	3.4	682	1 US-08-453-274B-107	Sequence 107, App
32	95.5	3.4	682	1 US-08-453-695A-107	Sequence 107, App
33	95.5	3.4	682	1 US-08-268-161A-107	Sequence 107, App
34	95.5	3.4	682	2 US-08-453-702A-107	Sequence 107, App
35	95.5	3.4	682	4 US-09-099-639-107	Sequence 107, App
36	95.5	3.4	682	5 PCT-US93-12588-107	Sequence 107, App
37	95.5	3.4	682	5 PCT-US95-08071-107	Sequence 107, App
38	95.5	3.4	836	1 US-07-998-003A-105	Sequence 105, App
39	95.5	3.4	836	1 US-08-453-274B-105	Sequence 105, App
40	95.5	3.4	836	1 US-08-453-695A-105	Sequence 105, App
41	95.5	3.4	836	1 US-08-268-161A-105	Sequence 105, App
42	95.5	3.4	836	2 US-08-453-702A-105	Sequence 105, App
43	95.5	3.4	836	5 US-09-099-639-105	Sequence 105, App
44	95.5	3.4	836	5 PCT-US93-12588-105	Sequence 105, App
45	95.5	3.4	836	5 PCT-US95-08071-105	Sequence 105, App

ALIGNMENTS

RESULT 1					
US-08-868-373-8					
Sequence 8, Application US/08868373					
Patent No. 6307128					
GENERAL INFORMATION:					
APPLICANT: JAWORSKI, Jan G.					
APPLICANT: Post-Belittenmiller, Martha A.					
TITLE OF INVENTION: FATTY ACID ELONGASIS					
FILE REFERENCE: 07148/064001					
CURRENT APPLICATION NUMBER: US/08/868, 373					
CURRENT FILING DATE: 1997-06-03					
NUMBER OF SEQ ID NOS: 22					
SOFTWARE: FASTSEQ for Windows Version 3.0					
SEQ ID NO 8					
LENGTH: 550					
TYPE: PRT					
ORGANISM: Arabidopsis thaliana					
US-08-868-373-8					
Query Match					
Best Local Similarity 99.9% Score 2845; DB 4; Length 550;					
Matches 549; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MGRSNEODLLSTELVNRGIEPSGPNAGSPTESVRRRLPDFLOSNEKYVGLGYHLIN	60		
DB	1	MGRSNEODLLSTELVNRGIEPSGPNAGSPTESVRRRLPDFLOSNEKYVGLGYHLIN	60		
QY	61	HAVYATIPVLVLFSAEVSLSREIWKIMDYDLATVIGFVFLTACYEFSRPRS	120		
DB	61	HAVYATIPVLVLFSAEVSLSREIWKIMDYDLATVIGFVFLTACYEFSRPRS	120		
QY	121	VYLIDFACVYKSDHKVKEEFIELARKSGKDEETLGFKKRILOASGIGDTPYPRIS	180		
DB	121	VYLIDFACVYKSDHKVKEEFIELARKSGKDEETLGFKKRILOASGIGDTPYPRIS	180		
QY	181	SEENITTKKEGHEASVYIFGALDELFEKTRVKKPDVGVLYVNCISFNPPTSLSAMVINH	240		
DB	181	SEENITTKKEGHEASVYIFGALDELFEKTRVKKPDVGVLYVNCISFNPPTSLSAMVINH	240		
QY	241	YKMGNIISYVNGMGCSAGITADLDMLOSNNSAVVSTVMGVNMYVSGDKSMV	300		
DB	241	YKMGNIISYVNGMGCSAGITADLDMLOSNNSAVVSTVMGVNMYVSGDKSMV	300		
QY	301	IPNCFRMGCSAVMISNRRPFRHAKYRLEHVRHKAADRSFVSVOEEDGEGFKLK	360		
DB	301	IPNCFRMGCSAVMISNRRPFRHAKYRLEHVRHKAADRSFVSVOEEDGEGFKLK	360		
QY	361	ISRDLMEVGEALKTNTITLGLVLPFSEQLFFFAALRRFSPAAKSTSTTSFSTSAVA	420		
DB	361	ISRDLMEVGEALKTNTITLGLVLPFSEQLFFFAALRRFSPAAKSTSTTSFSTSAVA	420		

Db 361. ISRDLMVEGBALKTNTITLGLPLVPSEQLLFFAALVYRRTSPAAKTSTTSTSTATA 420
 Oy 421. KTGKSSSSDLSKPYIPDYKLAHFHCFHAASKVYLEELOKNLGLSENNEMASRMTLHR 480
 Db 421. KTGKSSSSDLSKPYIPDYKLAHFHCFHAASKVYLEELOKNLGLSENNEMASRMTLHR 480
 Oy 481. FGNWSSGIVYELAYMAKSSVRGRDVMQJAFSGFKCSYVMAKRYKKPTPRNPV 540
 Db 481. FGNWSSGIVYELAYMAKSSVRGRDVMQJAFSGFKCSYVMAKRYKKPTPRNPV 540
 Oy 541. DCINRPPVPL 550
 Db 541. DCINRPPVPL 550

RESULT 2

US-08-868-373-14
 ; Sequence 14, Application US/08868373
 ; Patent No. 6307128
 ; GENERAL INFORMATION:
 ; APPLICANT: Jaworski, Jan G.
 ; APPLICANT: Post-Beltemmiller, Martha A.
 ; APPLICANT: Todd, James
 ; TITLE OF INVENTION: FATTY ACID ELONGASES
 ; FILE REFERENCE: 07148/064001
 ; CURRENT APPLICATION NUMBER: US/08/868,373
 ; CURRENT FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 14
 ; LENGTH: 516
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-08-868-373-14

Query Match 55.1%; Score 1569; DB 4; Length 516;
 Best Local Similarity 56.5%; Pred. No. 3.3e-155;
 Matches 300; Conservative 82; Mismatches 117; Indels 32; Gaps 5;

Oy 23. GPNAGSPFSYVRRLPDLQSVNLKYGHYHLINHAAYLATIPVLVFSAEVSL 82
 Db 13. GGGGDSVGVQJROTMLPDLQSVNLKYGHYHLINHAAYLATIPVLVFSAEVSL 71
 Oy 83. SREIWKRLM--DYDLATVIGFGVFLTACVYEMSRPRSVYLDFEACYPDSBHKYTK 139
 Db 72. NPDDL-KQLMHLQNLVLSIITCSAILVGLTIVMTRPRVYLVDFSCYLPBHLKAPY 130
 Oy 140. EEFELARKSGKDEDETLGFKRILQASIGDETYVPRSSISENITMKEGREASTVI 199
 Db 131. ARFMEHRLTGDFDSDSLFQKILERSGLGEDTYVPEAMHYVPRISMAAREBAEQVM 190
 Oy 200. FGALDELFEKTRVPRKGVYVNCSTFNPPLSLAMVINHYKRGNTLSYNGMGCSA 259
 Db 191. FGALDNLFPANTVAKPKDIGILVNCSTFNPPLSLAMVINHYKRGNTLSYNGMGCSA 250
 Oy 260. GIIAIDLARDMLQSNPNSYVAVVSTEMVGYNMVYGSOKSWIIPRCFIRMGCSAVMLSNRR 319
 Db 251. GVIALADLAKMLLVHRTYAVVSTEMITQNMIFGNKSMILPCLERVGSAAVLISNKS 310
 Oy 320. RDRRAKYRLHEHIVRTHKAADRSFRSVYOEDQGFKGKISIDLMVEGVALKTNTIT 379
 Db 311. RDRRSRYRLVHYVTRHGADKAFRCVYQEDDTGTGTVSLKDLMAIGELTKNTIT 370
 Oy 380. LGLPLVPFSQQLLFFAALLRRTFSPAAKTSTTSTSTATAKNGIKSSSSDLSKPYIPD 439
 Db 371. LGLPLVPISQQLLFFMTLV-----VKKLNGVAKYPIPD 404
 Oy 440. YKLAFHFCFHAASKVYLEELOKNLGLSENNEMASRMTLHRGNTSSGIVYELAYWEAK 499
 Db 405. FKLAFHFCIHAGRAVIDELEKNLQLSPVHYEASRMTLHRGNTSSGIVYELAYWEAK 464
 Oy 500. ESVRRGDRWQJAFSGFKCSYVMAKRYKKPTPRNPVVDINNYPPVPL 550

Db 465. GRMRGRNVQJAFSGFKCSAWEALRV-KPSNNSPWEDCIDKXYPVTL 514

RESULT 3

US-08-868-373-10
 ; Sequence 10, Application US/08868373
 ; Patent No. 6307128
 ; GENERAL INFORMATION:
 ; APPLICANT: Jaworski, Jan G.
 ; APPLICANT: Post-Beltemmiller, Martha A.
 ; APPLICANT: Todd, James
 ; TITLE OF INVENTION: FATTY ACID ELONGASES
 ; FILE REFERENCE: 07148/064001
 ; CURRENT APPLICATION NUMBER: US/08/868,373
 ; CURRENT FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 537
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-08-868-373-10

Query Match 52.4%; Score 1493; DB 4; Length 537;
 Best Local Similarity 52.6%; Pred. No. 3.1e-147;
 Matches 287; Conservative 103; Mismatches 116; Indels 40; Gaps 9;

Oy 12. TELVNRGIPSGPNAGSPFSYVRV---RRRLPDLQSVNLKYGHYHLINHAAYLAT 67
 Db 23. SEAMEANRP--VNGGS--VQIRTEENERRKLPNFIQSVNMKYGHYHLITLHFKCL 78
 Oy 68. IPLVLVFSAEVSLSREIWKRLM--DYDLATVIGFGVFLTACVYEMSRPRSVYLI 124
 Db 79. VPLVAVLTELSTLTTDLY-QIWLHLQNLVAFIFLSALAFISGVYIMSRPRSVYLV 136
 Oy 125. DEACKRPSDEHRYTEEFELARKSGKDEDETLGFKRILQASIGDETYVPRSSISEN 184
 Db 137. DVCYLPLPSLQVYKQKMDHKLIEDFNESLEFQKILERSGLGEETVLEALHCIPP 196
 Oy 165. ITTMEGDEBASTVIFGALDELFEKTRVPRKGVYVNCSTFNPPLSLAMVINHYKMR 244
 Db 197. RPTMAAREESQVWFGALDKLFENTKINPRDIGLVVNCSTFNPPLSLAMVINHYKMR 256
 Oy 245. GIIISYNGMGCSAGIIAIDLARDMLQSNPNSYVAVVSTEMVGYNMVYGSOKSWIIPNC 304
 Db 257. GNVKSFNIGMGCSAGVISTDLAKDMLQVHNTYAVVSTEMITQNMIFGNKSMILPNC 316
 Oy 305. FFRMGCSAVMLSNRRDPRRAKYRLHEHIVRTHKAADRSFRSVYOEDQGFKGKISRD 364
 Db 317. LFRVGSAILLSNKGKDRRSRYRLVHYVTRHGADKAFRCVYQEDDTGTGTVSLSKD 376
 Oy 365. LMEVGEALKTNTITLGLPLVPSEQLLFFAALLRRTFSPAAKTSTTSTSTATAKNG 424
 Db 377. LMAIAGALKRNIITTLPLVLPISQQLLFFMTLVTK----- 412
 Oy 425. IKSSSDLSKPYIPDYKLAHFHCFHAASKVYLEELOKNLGLSENNEMASRMTLHRGNT 484
 Db 413. KLFNSKL-KPYIPDFELADHFCIHAGRAVIDELEKNLQLSOTVHEASRMTLHRGNT 470
 Oy 485. SSGSIVYELAYWEAKESVRGRDVMQJAFSGFKCSYVMAKRYKKPTPRNPVDCIN 544
 Db 471. SSSSIVYELAYWEAKGKMRGRNVQJAFSGFKCSAVVAVLNNV-KPSVSSPWEDCID 529
 Oy 545. RYPPVPL 550
 Db 530. RYPPVPL 535

RESULT 4

US-08-868-373-12
 ; Sequence 12, Application US/08868373
 ; Patent No. 6307128
 ; GENERAL INFORMATION:

; APPLICANT: Jaworski, Jan G.
 ; APPLICANT: Post-Beltemiller, Martha A.
 ; APPLICANT: Todd, James
 ; TITLE OF INVENTION: FATTY ACID ELONGASES
 ; FILE REFERENCE: 07148/064001
 ; CURRENT APPLICATION NUMBER: US/08/868,373
 ; CURRENT FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 12
 ; LENGTH: 500
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-08-868-373-12

Query Match 50.8%; Score 1446.5; DB 4; Length 500;
 Best Local Similarity 53.3%; Pred. No. 2e-142;
 Matches 281; Conservative 94; Mismatches 11; Indels 41; Gaps 9;

QY 28 SPTFSVRRRLPDFLOSUNLKYKLYGYYLHNNAVYLATIPVLVFSAEVGSLSREI 87
 DB 1 SPTMP---QAPMEPSSSKKLYKLYGYYLHNNAVYLATIPVLVFSAEVGSLSREI 56
 QY 88 ---WKLMYDLYATYI--GFGVYVLACVYFMSRPSVYLIDFACYKPSDEHKYKKEF 142
 DB 57 LNWVNSL-QFDLYVQLCSFFVIFIST--VFMSKRPRTIYLDVYSCYKPPVTCRVPEF 113
 QY 143 IELARSGFDEETLGFKRRIIOASIGIDETVPRSSISENTTMMKEGEEASTVIFGA 202
 DB 114 MHSRIILKDKRVSVEQMRILERSGLGETCLPRAIHYPPTMDARSEAOVIFGA 173
 QY 203 LDELKTRKPRDVGVLVNCSIFNPPTSLSAMVINHYKMRGUILSYNLGMCAGIT 262
 DB 174 MDLFRKTLKRDVILVNCSLSPPTSLSAMVINHYKMRGUILSYNLGMCAGIT 223
 QY 263 AIDLADMLQSNPNSTAVVYVSTEMVGYVSDKSMVLPNCFRNGCSAVMLSNRRDF 322
 DB 234 SYDLADLLQVHNSNAIIVSTEIITPNYQGNERAMLLPNCLEFRMGAAIHMSNRSDR 293
 QY 323 RHAQYRLHEIVTRHKAADRSFRSVYQEDQEGFKGLKISDLMVEGELAKNTITLGP 382
 DB 294 WRKATKLSLHVRHGRADRSFYCYEQDEKSHVGINLSKDLMAIGELAKNTITIGP 353
 QY 383 LVLPSEQLLFFPAALL-RRTFSPAARTSTTSSTSAFAKTINGIKSSSDLSKPYIPDK 441
 DB 354 LVLPASQLLFLSLGRIFNPK-----WKPYIPDK 386
 QY 442 LAPEHFCFHAASKVYVLEELQKNLIGSEENMASRMTLHRRGNTSSSGIWEYELAMEAKES 501
 DB 387 LAPEHFCIHAGRAVIDELQKNLQJLSEHVEASRMTLHRRGNTSSSGIWEYELIESKGR 446
 QY 502 VRRGDVWQIAGSGGFKCNSVYWKAMRKPKPRNNPWDCINRYPV 548
 DB 447 MRGRDVWQIAGSGGFKCNSAVWKCMRTIKTP-KDGPWSDCIDRYPV 492

RESULT 5
US-09-058-947A-4

Sequence 4, Application US/09058947A

Patent No. 6274790

GENERAL INFORMATION:

APPLICANT: Kunst et al.

TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme

TITLE OF INVENTION: Involved in Very Long Chain Fatty Acid Synthesis

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klarquist Sparkman Campbell

ADDRESSEE: Leigh & Whinston, LLP

STREET: One World Trade Center, Suite

STREET: 1600, 121 S.W. Salmon Street

CITY: Portland

STATE: OR

COUNTRY: USA

; ZIP: 97204-2988
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Disk, 3.5-inch
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows NT
 ; SOFTWARE: Word97 & ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/058, 947A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/043, 831
 ; FILING DATE: April 14, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: David J. Earp, Ph.D.
 ; REGISTRATION NUMBER: 41,401
 ; REFERENCE/DOCKET NUMBER: 5493-50032/DJE
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (503) 226-7391
 ; TELEFAX: (503) 228-9446
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 497
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-058-947A-4

Query Match 50.7%; Score 1445; DB 4; Length 497;
 Best Local Similarity 53.9%; Pred. No. 2.9e-142;
 Matches 278; Conservative 93; Mismatches 107; Indels 38; Gaps 8;

QY 39 LPDFLOSUNLKYKLYGYYLHNNAVYLATIPVLVFSAEVGSLSREI---WKLMYD 95
 DB 6 MPESSSVKLYKLYGYYLHNNAVYLATIPVLVFSAEVGSLSREI---WKLMYD 63
 QY 96 LATVI--GFGVYVLACVYFMSRPSVYLIDFACYKPSDEHKYKKEFTELARKSGKD 153
 DB 64 LVQVLCSSFFVIFIST--VFMSKRPRTIYLDVYSCYKPPVTCRVPEFHSRLIKOK 121
 QY 154 EETLGFKRRIIOASIGIDETVPRSSISENTTMMKEGEEASTVIFGALDELPEKTRV 213
 DB 122 PKSVFQMRILERSGLGETCLPRAIHYPPTMDARSEAOVIFEAADDLEFKRTGK 181
 QY 214 PKDGVLVNCSIFNPPTSLSAMVINHYKMRGUILSYNLGMCAGITADLARDMLOS 273
 DB 182 PKDVLIVNCSLESPPTSLSAMVINHYKMRGUILSYNLGMCAGITADLARDMLOS 241
 QY 274 NPNSTAVVYVSTEMVGYVSDKSMVLPNCFRNGCSAVMLSNRRDFRHAQYRLHEIV 333
 DB 242 HPSNNAIIVSTEIITPNYQGNERAMLLPNCLEFRMGAAIHMSNRSDRRAKYSLSHV 301
 QY 334 RTHKAADRSFRSVYQEDQEGFKGLKISDLMVEGELAKNTITLGPVLVLPSEQL 393
 DB 302 RTHGADDSFYCYEQDEKSHVGINLSKDLMAIGELAKNTITIGPLVLPASQL 361
 QY 394 FAALL-RRTFSPAARTSTTSSTSAFAKTINGIKSSSDLSKPYIPDYKLAPEHFCFHA 452
 DB 362 LTLGRIKIFNPK-----WKPYIPDKLAFHFCFHA 394
 QY 453 SKVLEELQKNLIGSEENMASRMTLHRRGNTSSSGIWEYELAMEAKESVRRGRDWOJA 512
 DB 395 GRAVIDELQKNLQJLSEHVEASRMTLHRRGNTSSSGIWEYELIESKGRARRRDRWOJA 454
 QY 513 FGSQFRCNSVYWKAMRKPKPRNNPWDCINRYPV 548
 DB 455 FGSQFRCNSAVWKCMRTIKTP-KDGPWSDCIDRYPV 489

RESULT 6
 US-08-868-373-2
 ; Sequence 2, Application US/08868373
 ; Patent No. 6307128

US-08-868-373-4
Sequence 4, Application US/08868373
Patent No. 6307128
GENERAL INFORMATION:
APPLICANT: JAWORSKI, Jan G.
APPLICANT: Post-Baltenmiller, Martha A.
APPLICANT: Todd, James
TITLE OF INVENTION: FATTY ACID ELONGASES
FILE REFERENCE: 01148/064001
CURRENT APPLICATION NUMBER: US/08/868,373
CURRENT FILING DATE: 1997-06-03

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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/888,998
FILING DATE: 07-JUL-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,603
FILING DATE: 26-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 12176-004300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 506 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..506
OTHER INFORMATION: /note="Amino acid sequence of FAE1
US-08-888-998-2

Query Match 41.6%; Score 1186; DB 3; Length 506;
Best Local Similarity 45.5%; Pred. No. 3,7e-115;
Matches 238; Conservative 87; Mismatches 150; Indels 48; Gaps 6;

QY 43 LOSVNLKVKLYHLYNHAVYLAIPVLYVFSAEVGSLSREEL-----WKLMYDYL 97
DB 1 MTSVN---VKLLYRVLYLNFENLCLPLTAFL---AKASRLTINDLHNLSTYQHNL 53
QY 98 TWIGFGEVFLTACVYMSRPSRYLLIDFACYKPSDEHKYKEETEL-----AR 147
DB 54 TVTLFAVYVGLVLYITRPNPYLVDSYCLPPHLKVSVMDFYQIRKADTSR 113
QY 148 KSGFDEETLGFKRRILOASGIGDETYVPRSSISSENTITTKEGREASTYIFGALDEL 207
DB 114 NVACDDPSLDFLKRIGERSGLGETYSPEGLIHVPPRKYPAASRETEKYIALENLF 173
QY 208 EKTAVKPKDVGVLVNCISFNPPTSLSAMVINHYKMGNIISYNLGCGCSAGIATDIA 267
DB 174 ENTAVNPREIGILVYNSMFPPTSLSAMVINHYKMGNIISYNLGCGCSAGIATDIA 233
QY 268 RDLQSNPNSTAVVYSTEMGYNMYVGSCKSMVIPNCFEFGKCSAVMLSNRRDPRHAKY 327
DB 234 KDLHVHKNYVALVYSTENITQGIYAGENRSMVSNCLFVGAAILLSNKGDRRSKY 293
QY 328 RLEHIVTRHKAADRSFRSVYQEDDEGFKLAKSRDLMEVGERLAKNTITTLPLVLPF 387
DB 294 KLVHTVTRHGADKSRFCVQOEDDESGKIGVCLSKDITVNAAGTTLTKNATLPLPL 353
QY 388 SEQLLFPALRLRTFSPAATSTTSTSTATKTNGIKSSSSDLSKPYIDYKLAPEHF 447
DB 354 SEKLFPAFTFAK-----KLLKDKIKHYYVDFELANDHF 388
QY 448 CFHAAKSVYLELOKNTGLSENNKASBMTLHRTGNTSSGSIWELAYMEAKESVRGRDR 507
DB 389 CIIHAGGAVVIDELKKNGLSPIDVEASRSTLHRTGNTSSSISWELAYIEAKGMKGNK 448
QY 508 VMOAFSGFKCNSTVWKKAMKRYKPTIRNNPNVDCINRYPPL 550
DB 449 AMOIALSGFKCNSTVWKKAMKRYKPTIRNNPNVDCINRYPPL 490

RESULT 9
US-09-362-633-2
; Sequence 2, Application US/09362633
; Patent No. 6184355
; GENERAL INFORMATION:

APPLICANT: JAMES, Douglas W.
APPLICANT: LIM, Eda
APPLICANT: KELLER, Janis
APPLICANT: DOONER, Hugo K.
TITLE OF INVENTION: FAE1 GENES AND THEIR USES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,633
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,998
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 12176-004300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 506 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..506
OTHER INFORMATION: /note="Amino acid sequence of FAE1
US-09-362-633-2

Query Match 41.6%; Score 1186; DB 4; Length 506;
Best Local Similarity 45.5%; Pred. No. 3,7e-115;
Matches 238; Conservative 87; Mismatches 150; Indels 48; Gaps 6;

QY 43 LOSVNLKVKLYHLYNHAVYLAIPVLYVFSAEVGSLSREEL-----WKLMYDYL 97
DB 1 MTSVN---VKLLYRVLYLNFENLCLPLTAFL---AKASRLTINDLHNLSTYQHNL 53
QY 98 TWIGFGEVFLTACVYMSRPSRYLLIDFACYKPSDEHKYKEETEL-----AR 147
DB 54 TVTLFAVYVGLVLYITRPNPYLVDSYCLPPHLKVSVMDFYQIRKADTSR 113
QY 148 KSGFDEETLGFKRRILOASGIGDETYVPRSSISSENTITTKEGREASTYIFGALDEL 207
DB 114 NVACDDPSLDFLKRIGERSGLGETYSPEGLIHVPPRKYPAASRETEKYIALENLF 173
QY 208 EKTAVKPKDVGVLVNCISFNPPTSLSAMVINHYKMGNIISYNLGCGCSAGIATDIA 267
DB 174 ENTAVNPREIGILVYNSMFPPTSLSAMVINHYKMGNIISYNLGCGCSAGIATDIA 233
QY 268 RDLQSNPNSTAVVYSTEMGYNMYVGSCKSMVIPNCFEFGKCSAVMLSNRRDPRHAKY 327
DB 234 KDLHVHKNYVALVYSTENITQGIYAGENRSMVSNCLFVGAAILLSNKGDRRSKY 293
QY 328 RLEHIVTRHKAADRSFRSVYQEDDEGFKLAKSRDLMEVGERLAKNTITTLPLVLPF 387
DB 294 KLVHTVTRHGADKSRFCVQOEDDESGKIGVCLSKDITVNAAGTTLTKNATLPLPL 353

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OY 388 SEQLLFPALLRRTSPDAKTSTTTSFSTATAKNGIKSSSDLSKPIPYDLAEHF 447
DB 354 SEKLEFPAFVAK-----KLLKKIKHYVPDKLAVDHF 368
OY 448 CFHAAKSVYLEEOKNLGISEENMEASRMTLHREFGTSSSGIYELAYMEAKESVRGDR 507
DB 389 CHAGRAVAYDELEKMLGSPIDVEASRSTLHREFGTSSSGIYELAYTEAKGRMKGNK 448
OY 508 WMOIAGSGFKCNSVYKAMRKVKKPTNNPWCINRYVPVL 550
DB 449 AMOIALGSGFKCNSAVVALRVN-KASANSPMQHCIDRIPVKI 490

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RESULT 10

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US-08-868-373-6
; Sequence 6, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868,373
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-868-373-6

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Query Match 41.1%; Score 1170.5; DB 4; Length 504;
Best Local Similarity 48.8%; Pred. No. 1.5e-113;
Matches 227; Conservative 75; Mismatches 126; Indels 37; Gaps 4;

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OY 95 DLAVVIGFVGLVLAQYFMSRPSRYLLDPACPKPSDEHVKTEEFIELARKS----- 149
DB 66 NLQITISLLFLVFWLWILYMLTRKRPVYLVDSCYLPKSHLKVSIQTLMGHARRAREGM 125
OY 150 ---GKPEETLGFKKRILOASGIDENYVPSISSEITTMKGREASVITGALDEL 206
DB 126 CMKKESDHLVDFOEKILERSGLOEYIIPGLOCPLOOGGASRRETEEVIGALDNL 185
OY 207 PEKTRVAPKDVGLVNCISIFNPTPSLAVINHYKMRGNILSYNLGMSGAGITIDL 266
DB 186 FRNTGVKPDIGILVNSSTFNPTPSLASMIVNKKLRDNKISNLGMSGAGIYADV 245
OY 267 ARDMLGSPNSAVVSTENAVGYGSDKSNVTPNCFRMSGSAVMLSNRRDRFRAK 326
DB 246 AKGILQVHRTVYALVSTENITONLYGKNKSMILVNCILFRVGAVALLSNRSRDRRAK 305
OY 327 YLEHYVTRTKAADRSFRSVYOEDEOGFGKLSRDLMVEGGEALKTITTLGPLVLP 366
DB 306 YELVHYVRIHTGSDDSFEGATOEDEBDGIIQVTLKRNLMVAVARLKIINATLGPLVLP 365
OY 387 FESQQLFPAALLRRT-FSPAAKTSTTTSFSTATAKNGIKSSSDLSKRYIDYKLAPE 445
DB 366 LKEKLAFFITFVKKYKFKPELRN-----YTPDFKLAPE 398
OY 446 HRCFHAASKVYLEEOKNLGISEENMEASRMTLHREFGTSSSGIYELAYMEAKESVRG 505
DB 399 HECIHAGGALIDELKKNKLSPLHVEASRMTLHREFGTSSSGIYELAYTEAKGRMKGN 458
OY 506 DRVMOIAGSGFKCNSVYKAMRKVKKPTNNPWCINRYVPVL 550
DB 459 DRIWOIAGSGFKCNSVVALRVN-KPSANSPEWDCMDRYPEI 502

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RESULT 11

US-08-888-998-4

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; Sequence 4, Application US/08888998
; Patent No. 6124324
; GENERAL INFORMATION:
; APPLICANT: JAMES, Douglas W.
; APPLICANT: LIM, Eda
; APPLICANT: KELLER, Janis
; APPLICANT: DOONER, Hugo K.
; TITLE OF INVENTION: FAEL GENES AND THEIR USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,998
; FILING DATE: 07-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,603
; FILING DATE: 26-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 12176-004300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; FEATURE:
; MOLECULE TYPE: peptide
; NAME/KEY: Protein
; LOCATION: 1..116
; OTHER INFORMATION: /note="partial amino acid sequence
; OTHER INFORMATION: of B. napus FAEL protein"
US-08-888-998-4

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Best Local Similarity 44.4%; Pred. No. 5e-27;
Matches 68; Conservative 22; Mismatches 37; Indels 26; Gaps 2;

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OY 334 RTHKAADRSFRSVYOEDEOGFGKLSRDLMVEGGEALKTITTLGPLVLPFSQLLF 393
DB 1 RTHGADDKFRVCOGDDENGKIGVSLSDITDVAGRTVKNRIATLGPLILPSKLLF 60
OY 394 FALLRRTSPAAKTSTTTSFSTATAKNGIKSSSDLSKPYIPYKLAHFECFHAAS 453
DB 61 FVTFM-----GKLFKDKIKHYVPDKLAIDHFCIH-RS 94
OY 454 KYVLEELQKNLIGISEENMEASRMTLHREFGTSS 486
DB 95 RAVIDVLEKRLAPIDVEASRSTLHREFGNTSS 127

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RESULT 12

US-09-362-633-4

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; Sequence 4, Application US/09362633
; Patent No. 6184355
; GENERAL INFORMATION:
; APPLICANT: JAMES, Douglas W.
; APPLICANT: LIM, Eda

```

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TITLE OF INVENTION: Plant Root Diseases
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Margaret A. Connor, Patent Advisor
STREET: 800 Buchanan St
CITY: Albany
STATE: CA
COUNTRY: USA
ZIP: 94710
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/994,035C
FILING DATE: 18-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Connor, Margaret A
REGISTRATION NUMBER: 30,043
REFERENCE/DOCKET NUMBER: 0009, 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 559 6067
TELEFAX: (510) 559 5736
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-994-035C-5

Query Match 6.0%; Score 169.5; DB 4; Length 349;
Best Local Similarity 21.8%; Pred. No. 4,4e-09;
Matches 90; Conservative 61; Mismatches 173; Indels 89; Gaps 15;

QY 130 KPS---DEKVTKEEFIELARKSGKFEDETTGFKRRILOASGIGDETYVPSIS----- 180
    ||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 6 KPSLTFPHYKTIQOQMIDHLEQLHD-DHPRMALARKMIQNTQV-NERYLVLPIDELAVHT 63

QY 181 ---SSNITTMMEGREASTVIFGALDELFEKTRVYKPYVG-VLVNCSIFNFTPSLSANV 237
    ||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 64 GFTHSIYEREARMSI---AARQAIENAGLTTDDIRMAVVSICGE-MPISLTAHL 118

QY 238 INHYKRGNIISYNLGSGCSAGIIAIDLARDMLQSNPSYAVVSTEMVGYNMYVGS DK 297
    ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 119 INDGLKRSITYQLPTAIOJQCVAGAALINRANFALSLSPNHALIYLSLESSL-CYQPODT 177

QY 298 SM-VIPNCFPRMCCSAVMLSNRRDPFRHAKYRLHEIVFTHKADDRSFRSYQDEDEG 355
    ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 178 KLHAFISALTEGDAVASACVM-----RADDKA-----PG 205

QY 356 FKGLKISIDLMEVGEALKTNTITGLPLVPSSEDLFPFALLKRTFSPAATSTTTTSS 415
    ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 206 FK-----IAKTGSYFLPDSHYIY-----DYKDSGEHF 234

QY 416 TSAFTKNGIKSSS---SDLKPYIPDYKLAIEHFCFPAASKVYLELOKNTGLSEENME 472
    ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 235 TLDAVYMSIKDYAPAMEELNFEFTNQCAQNDFFIFHTGSKKIIDLDELVALQDLDPGRA 294

QY 473 ASRMTLHRRFTSSSGIWEELAYMEAKESVRRGRVWOVIAFGSGFKCNSVYRK 525
    ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 295 QSRDLSLSEAGNIASY-VVEVDVLRQFDGSGPANGATGMLAALFPGPTAEAVYAK 346

RESULT 14
US-09-395-861-5
; Sequence 5, Application US/09395861
; Patent No. 6447770
; GENERAL INFORMATION:
; APPLICANT: Raaijmakers, Jos M
; APPLICANT: Weller, David M

```

```

; APPLICANT: Thomashow, Linda S
; APPLICANT: Cook, R James
; TITLE OF INVENTION: Biocontrol Agents for Take-All
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Margaret A. Connor, USDA-ARS
; STREET: 800 Buchanan Street
; CITY: Albany
; STATE: CA
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/395,861
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,938
; FILING DATE: 20-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Connor, Margaret A
; REGISTRATION NUMBER: 30043
; REFERENCE/DOCKET NUMBER: 0027.97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 559-6067
; TELEFAX: (510) 559-5736
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-395-861-5

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Query Match      6.08; Score 169.5; DB 4; Length 349;
Best Local Similarity 21.88; Pred. No. 4.4e-09;
Matches 90; Conservative 61; Mismatches 173; Indels 89; Gaps 15;

QY 130 KPS---DEHKVTKREFTEELAKSKSKFDEETLGFKKRILOASGIDEYTPRSIS-----180
Db 6 KPSLLFPHYKTIQOQMDHLEQLHD-DHPRALAKRMIONOV-NERYLVPIDELAVHT 63

QY 181 --SSENTITMKEGEEASTVIFGALDELFEKTRVYKPDVG-VLVVNCISIFNPPTSAMV 237
Db 64 GFTHRSIVYEREARMSI-----AARQAIENAGLTDDIRWAVTSGTF-MMPSTLAHL 118

QY 238 INHYKMGNTLSYNLGSGSAGIIAIDLARDMLQSPNSYAVVSTEMGYNNYVGS DK 297
Db 119 INDLGLTSTVOLPIAQLGCVAGAAINRANDFASLSPDNHALVLSLEFSSL-CYQPDPT 177

QY 298 SM--VIPNCFEFGGCSAVMLSNRRDRFRAKYRLEHIVRTHKAADDSFSVYQEEDEOG 355
Db 178 KLAFAISALFGDAVSACV-----RADDKA-----PG 205

QY 356 FKGLKISRDLMEVGEALKNITTLGVLVPSFQQLFFAALLRTPSPAKTSTTSPS 415
Db 206 FK-----IAKTGSYFLPDSHHYIKY-----DYKDSGFHF 234

QY 416 TSATATNGIKSSS---SDLSKPYIPDYKLAFFHFCFHAASKVYLELOKNGLSEENME 472
Db 235 TLDKAYMNSIKVAPMMEELNETFNQCAQNDFFTFHGGKRIIDELVQLDLEGRVA 294

QY 473 ASRMTLHRRGNTSSSGIWEIAYMEAKESVRGRDRWQJAFSGGFNCNSVYWK 525
Db 295 QSRDSLSEAGNTASV-VVFDVLKRPDSDGPANGATGMLAFAFGPFAEMA V GK 346

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; Sequence 12, Application US/08494907
; Patent No. 595298
; GENERAL INFORMATION:
; APPLICANT: Thomashow, Linda S
; APPLICANT: Bangera, Mahalaxmi
; APPLICANT: Weller, David M
; APPLICANT: Cook, R. James
; TITLE OF INVENTION: Sequences for Production of
; NUMBER OF SEQUENCES: 20
; TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and Methods
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Margaret A. Connor, USDA-ARS
; STREET: 800 Buchanan Street
; CITY: Albany
; STATE: CA
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,907
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Connor, Margaret A
; REGISTRATION NUMBER: 30043
; REFERENCE/DOCKET NUMBER: 0009.95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 559-5777
; TELEFAX: (510) 559-6067
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-494-907-12

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Query Match      5.88; Score 166.5; DB 2; Length 349;
Best Local Similarity 21.88; Pred. No. 9.1e-09;
Matches 90; Conservative 61; Mismatches 173; Indels 89; Gaps 15;

QY 130 KPS---DEHKVTKREFTEELAKSKSKFDEETLGFKKRILOASGIDEYTPRSIS-----180
Db 6 KPSLLFPHYKTIQOQMDHLEQLHD-DHPRALAKRMIONOV-NERYLVPIDELAVHT 63

QY 181 --SSENTITMKEGEEASTVIFGALDELFEKTRVYKPDVG-VLVVNCISIFNPPTSAMV 237
Db 64 GFTHRSIVYEREARMSI-----AARQAIENAGLTDDIRWAVTSGTF-MMPSTLAHL 118

QY 238 INHYKMGNTLSYNLGSGSAGIIAIDLARDMLQSPNSYAVVSTEMGYNNYVGS DK 297
Db 119 INDLGLTSTVOLPIAQLGCVAGAAINRANDGSSLPDNHALVLSLEFSSL-CYQPDPT 177

QY 298 SM--VIPNCFEFGGCSAVMLSNRRDRFRAKYRLEHIVRTHKAADDSFSVYQEEDEOG 355
Db 178 KLAFAISALFGDAVSACV-----RADDKA-----PG 205

QY 356 FKGLKISRDLMEVGEALKNITTLGVLVPSFQQLFFAALLRTPSPAKTSTTSPS 415
Db 206 FK-----IAKTGSYFLPDSHHYIKY-----DYKDSGFHF 234

QY 416 TSATATNGIKSSS---SDLSKPYIPDYKLAFFHFCFHAASKVYLELOKNGLSEENME 472
Db 235 TLDKAYMNSIKVAPMMEELNETFNQCAQNDFFTFHGGKRIIDELVQLDLEGRVA 294

QY 473 ASRMTLHRRGNTSSSGIWEIAYMEAKESVRGRDRWQJAFSGGFNCNSVYWK 525
Db 295 QSRDSLSEAGNTASV-VVFDVLKRPDSDGPANGATGMLAFAFGPFAEMA V GK 346

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Mon May 12 16:41:41 2003

us-09-905-657-2.rai

Page 9

Search completed: May 10, 2003, 23:54:33
Job time : 240 secs

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OM protein - protein search, using sw model

Run on: May 10, 2003, 22:53:14 ; Search time 1217 Seconds

(Without alignments)
93.119 Million cell updates/sec

Title: US-09-905-657-2

Perfect score: 2848

Sequence: 1 MGRSNGDLSTETVNRGIE.....KKPTRRNPWDCINRPVPL 550

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriaph:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2840	99.7	550	10	091LE5
5	2605	91.5	508	10	091LE6
6	2324	81.6	535	10	08VWP9
7	2175.5	76.4	526	10	08S2K3
8	2005	70.4	389	10	091LE7
9	1820	63.9	352	10	091LE3
10	1784	62.6	351	10	091LE6
11	1569	55.1	516	10	091LE9
12	1494.5	52.5	509	10	048780
13	1492	52.4	512	10	09S1X1
14	1476.5	51.8	513	10	09FXZ8
15	1470.5	51.6	505	10	09FW67
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17	1452	51.0	523	10	08VWX2	08VWX2 arabidopsis
18	1447	50.8	517	10	081658	081658 hemerocalli-
19	1445	50.7	497	10	09XF43	09XF43 arabidopsis
20	1443	50.7	529	10	09F687	09F687 arabidopsis
21	1443	50.7	529	10	094CA1	094CA1 arabidopsis
22	1441	50.6	528	10	09MAM3	09MAM3 arabidopsis
23	1439	50.5	497	10	08VYJ5	08VYJ5 arabidopsis
24	1438	50.5	520	10	09ZTK3	09ZTK3 arabidopsis
25	1435	50.4	521	10	041301	041301 simmondsia
26	1402	49.2	487	10	065677	065677 arabidopsis
27	1397	49.1	503	10	08RXA6	08RXA6 tropaeolum
28	1372	48.2	492	10	09C6L5	09C6L5 arabidopsis
29	1316	46.2	598	10	094C75	094C75 oryza sativ
30	1215.5	42.7	532	10	09XEP1	09XEP1 sorghum bic
31	1213	42.6	451	10	09SUY9	09SUY9 arabidopsis
32	1205	42.3	506	10	08S3A2	08S3A2 brassica ol
33	1203	42.2	506	10	08S3A3	08S3A3 brassica na
34	1201	42.2	496	10	093XD5	093XD5 lequerella
35	1197.5	42.0	505	10	093J10	093J10 brassica na
36	1196.5	42.0	466	10	09ZU20	09ZU20 arabidopsis
37	1194	41.9	493	10	09SYZ0	09SYZ0 arabidopsis
38	1189	41.7	506	10	08S3A1	08S3A1 brassica ca
39	1188	41.7	506	10	093XF0	093XF0 brassica na
40	1186	41.6	506	10	038860	038860 arabidopsis
41	1181	41.5	506	10	08S3A0	08S3A0 brassica na
42	1180	41.4	506	10	023738	023738 brassica na
43	1170.5	41.1	476	10	09ZUK2	09ZUK2 arabidopsis
44	1154	40.5	621	10	09AXE6	09AXE6 dunaliella
45	1151.5	40.4	459	10	09SS39	09SS39 arabidopsis

ALIGNMENTS

RESULT 1

064846 ID 064846 PRELIMINARY; PRT; 550 AA.
AC 064846:
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative beta-ketoacyl-CoA synthase (FIDDLEHEAD protein)
DE (AT2G26250/TID16.11).
DE TID16.11 OR FDH
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Yephremov A., Wisman E., Huijser P., Huijser C., Wellesen K.,
RA Siedler H.;
RT "The FIDDLEHEAD gene, which mutation results in graft-like surface
RT tissue fusions in Arabidopsis thaliana, encodes an epidermis specific
RT condensin enzyme of lipid metabolism.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. LANDSBERG ERRECTA;
RA MEDLINE=20122614; PubMed=10655527;
RA Pruitt R.E., Vielle-Calzada J.P., Ploense S.E., Grossniklaus U.,
RA Lohle S.J.;
RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
RT in Arabidopsis, encodes a putative lipid biosynthetic enzyme.";

Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).

[4] SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinozaki K., Shinozaki A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.,
 RT "Full length cDNA of gene TID16.11/At2g26250 (GI:3075394).";
 RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Shinozaki A.,
 RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
 RA Davis R.W., Theologis A., Ecker J.R.,
 RT "Arabidopsis cDNA clones";
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC004484; AAC14526.1;
 DR EMBL: AJ010713; CA003111.1;
 DR EMBL: AF214490; AAF73973.1;
 DR EMBL: AF214489; AAF73973.1; JOINED.
 DR EMBL: AF337910; AAG60062.1;
 DR EMBL: AY039563; AAK62618.1;
 DR InterPro: IPR01099; N-C-synthase.
 DR Pfam: PF02797; Chal_stl_synthc.1.
 DR Prodom: PD000453; N-C-synthase; 2.
 SQ SEQUENCE 550 AA; 61961 MW; 5DB3368601EDF174 CRC64;

Query Match 100.0%; Score 2848; DB 10; Length 550;
 Best Local Similarity 100.0%; Pred. No. 7.5e-228;
 Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSNDOLLSTETVNRGIEPSGNAGSPFVSVRRLPDLQSVNLYKYLGHYLYN 60
 DB 1 MGRSNDOLLSTETVNRGIEPSGNAGSPFVSVRRLPDLQSVNLYKYLGHYLYN 60
 QY 61 HAVLATIPVLVYFSAVGSLSREETWKLMVDLATVIGFGVYLTACVYFMSRPRS 120
 DB 61 HAVLATIPVLVYFSAVGSLSREETWKLMVDLATVIGFGVYLTACVYFMSRPRS 120
 QY 121 VYLDFACYRPSDEHKYTKKEEFIELARKSGFDEETLGFKRRIQASGIGDETVPRSS 180
 DB 121 VYLDFACYRPSDEHKYTKKEEFIELARKSGFDEETLGFKRRIQASGIGDETVPRSS 180
 QY 181 SSENITTMKGRREASVIFGALDELFEKTRVPRKDVGLVNVCSINPTPSLSAMYINH 240
 DB 181 SSENITTMKGRREASVIFGALDELFEKTRVPRKDVGLVNVCSINPTPSLSAMYINH 240
 QY 241 YKRGNTLSYNLGMCSSAGITAIIDLARDMLQSNPNSYAVVSTENGYMNYGSDKSMY 300
 DB 241 YKRGNTLSYNLGMCSSAGITAIIDLARDMLQSNPNSYAVVSTENGYMNYGSDKSMY 300
 QY 301 IPNCFRPMGCSAVMLNRRRDPFHAKYRLHIVTRTKAADRSFRSYOEDEQGFGLK 360
 DB 301 IPNCFRPMGCSAVMLNRRRDPFHAKYRLHIVTRTKAADRSFRSYOEDEQGFGLK 360
 QY 361 ISRDLMVEGGEALKTNTITLGLPLVLPFSQDLFFAALLRRTSPAKTSTTTSFSATATA 420
 DB 361 ISRDLMVEGGEALKTNTITLGLPLVLPFSQDLFFAALLRRTSPAKTSTTTSFSATATA 420
 QY 421 KNGIKSSSSDSDSKPIPYKLAFEHFCFHAASKVYLEELQNLGLSEENMASRMTLHR 480
 DB 421 KNGIKSSSSDSDSKPIPYKLAFEHFCFHAASKVYLEELQNLGLSEENMASRMTLHR 480
 QY 481 FGNITSSGIWELAYMEAKESVRRGDRVQIAFGSGFCNSVYVWAMRKVKKPTRRNPV 540
 DB 481 FGNITSSGIWELAYMEAKESVRRGDRVQIAFGSGFCNSVYVWAMRKVKKPTRRNPV 540

DB 481 FGNITSSGIWELAYMEAKESVRRGDRVQIAFGSGFCNSVYVWAMRKVKKPTRRNPV 540
 QY 541 DCINNYPPVL 550
 DB 541 DCINNYPPVL 550

RESULT 2
 ID 09LE4
 AC 09LE4; PRELIMINARY; PRT; 550 AA.
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-JUN-2002 (TREMBlrel. 15, Last sequence update)
 DE Fiddlehead protein.
 GN FHL.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20122614; PubMed=10655527;
 RA Pruitt R.E., Velle-Calzada J.P., Ploense S.E., Grossniklaus U.,
 RA Lolle S.J.;
 RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 in Arabidopsis, encodes a putative lipid biosynthetic enzyme.";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
 DR EMBL: AF214504; AAF73980.1;
 DR EMBL: AF214503; AAF73980.1; JOINED.
 DR InterPro: IPR01099; N-C-synthase.
 DR Pfam: PF02797; Chal_stl_synthc.1.
 DR Prodom: PD000453; N-C-synthase; 2.
 SQ SEQUENCE 550 AA; 61960 MW; 53BD368601E75174 CRC64;

Query Match 99.9%; Score 2844; DB 10; Length 550;
 Best Local Similarity 99.8%; Pred. No. 1.6e-227;
 Matches 549; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSNDOLLSTETVNRGIEPSGNAGSPFVSVRRLPDLQSVNLYKYLGHYLYN 60
 DB 1 MGRSNDOLLSTETVNRGIEPSGNAGSPFVSVRRLPDLQSVNLYKYLGHYLYN 60
 QY 61 HAVLATIPVLVYFSAVGSLSREETWKLMVDLATVIGFGVYLTACVYFMSRPRS 120
 DB 61 HAVLATIPVLVYFSAVGSLSREETWKLMVDLATVIGFGVYLTACVYFMSRPRS 120
 QY 121 VYLDFACYRPSDEHKYTKKEEFIELARKSGFDEETLGFKRRIQASGIGDETVPRSS 180
 DB 121 VYLDFACYRPSDEHKYTKKEEFIELARKSGFDEETLGFKRRIQASGIGDETVPRSS 180
 QY 181 SSENITTMKGRREASVIFGALDELFEKTRVPRKDVGLVNVCSINPTPSLSAMYINH 240
 DB 181 SSENITTMKGRREASVIFGALDELFEKTRVPRKDVGLVNVCSINPTPSLSAMYINH 240
 QY 241 YKRGNTLSYNLGMCSSAGITAIIDLARDMLQSNPNSYAVVSTENGYMNYGSDKSMY 300
 DB 241 YKRGNTLSYNLGMCSSAGITAIIDLARDMLQSNPNSYAVVSTENGYMNYGSDKSMY 300
 QY 301 IPNCFRPMGCSAVMLNRRRDPFHAKYRLHIVTRTKAADRSFRSYOEDEQGFGLK 360
 DB 301 IPNCFRPMGCSAVMLNRRRDPFHAKYRLHIVTRTKAADRSFRSYOEDEQGFGLK 360
 QY 361 ISRDLMVEGGEALKTNTITLGLPLVLPFSQDLFFAALLRRTSPAKTSTTTSFSATATA 420
 DB 361 ISRDLMVEGGEALKTNTITLGLPLVLPFSQDLFFAALLRRTSPAKTSTTTSFSATATA 420
 QY 421 KNGIKSSSSDSDSKPIPYKLAFEHFCFHAASKVYLEELQNLGLSEENMASRMTLHR 480
 DB 421 KNGIKSSSSDSDSKPIPYKLAFEHFCFHAASKVYLEELQNLGLSEENMASRMTLHR 480
 QY 481 FGNITSSGIWELAYMEAKESVRRGDRVQIAFGSGFCNSVYVWAMRKVKKPTRRNPV 540
 DB 481 FGNITSSGIWELAYMEAKESVRRGDRVQIAFGSGFCNSVYVWAMRKVKKPTRRNPV 540

Db 481 FGNFSSSGITWELIYMAKAKESVRGDRWQJALSGSGKCSVYAKAKRKYKPPTRNNPW 540

QY 541 DCINRYPVPL 550
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|||||

Db 541 DCINRYPVPL 550

RESULT 3	
Q9LLE8	
ID Q9LLE8	PRELIMINARY; PRT; 550 AA

DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Fladdhead protein.
GN FDI.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_Taxid=3702;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE-20122614; Pubmed-10655527;
RA Pruitt R.E., Vielle-Calzada J.P., Ploense S.E., Grossniklaus U.,
RA Iolte S.J.;
RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
RT in Arabidopsis, encodes a putative lipid biosynthetic enzyme".
RT Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
DR EMBL: AF214496; AAF73976.1; U00000.
DR EMBL: AF214495; AAF73976.1; JOINED.
DR InterPro: IPR001099; N-C-synthase.
DR Pfam: PF02797; Chai_still_synnc; 1.
DR PfDom: PD000453; N-C-synthase; 2.
SQ SEQUENCE 550 AA; 62019 MW; 5DB336860310DEA4 CRC64;

Query Match	99.8%	Score 2841	DB 10	Length 550
Best Local Similarity	99.8%	Pred. 2.9e-227		
Matches 549	Conservative 0	Mismatches 1	Indels 0	Gaps 0

Qy	1	MGRNEDDLSTELVYNGTIEPSGNGNASPFYSVYRRRLDPFLOSVMKTKVYKGLHYLIN	60
Db	1	MGRNEDDLSTELVYNGTIEPSGNGNASPFYSVYRRRLDPFLOSVMKTKVYKGLHYLIN	60
Qy	61	HAYLATIPVLVYVSAEVSGLSREELTWKIMDYDLATVIGFEGEVLTACVYFMSRPRS	120
Db	61	HAYLATIPVLVYVSAEVSGLSREELTWKIMDYDLATVIGFEGEVLTACVYFMSRPRS	120
Qy	121	VYLLDFPCYRSDSHKTKKEFTILARKSGFDEETLGFKRILQASGIDETVYPSIS	180
Db	121	VYLLDFPCYRSDSHKTKKEFTILARKSGFDEETLGFKRILQASGIDETVYPSIS	180
Qy	181	SSENITTWKREGEAREASTYIFGALDELFEKTEVKRKDVGLVAVNGSINPTPSLSAMYINH	240
Db	181	SSENITTWKREGEAREASTYIFGALDELFEKTEVKRKDVGLVAVNGSINPTPSLSAMYINH	240
Qy	241	YKMGNTILSYVLGMSGAGIITADLARDMLQSPNSYAVVYSTEWGYMYVGSDKSMV	300
Db	241	YKMGNTILSYVLGMSGAGIITADLARDMLQSPNSYAVVYSTEWGYMYVGSDKSMV	300
Qy	301	IPNCFPMGCSAVMLSNRRDPFRHAKTKRLEIYVTHKAADRSRSYOEDEDEGFGGLK	360
Db	301	IPNCFPMGCSAVMLSNRRDPFRHAKTKRLEIYVTHKAADRSRSYOEDEDEGFGGLK	360
Qy	361	ISRDLMVEYGALNTNITTLGPTLVLPFSEQLLFFPALRLRTFSPAATSTTTSSTGATA	420
Db	361	ISRDLMVEYGALNTNITTLGPTLVLPFSEQLLFFPALRLRTFSPAATSTTTSSTGATA	420
Qy	421	KTNIGKSSSSDLSKRPYIPDYKLAIEHHCFFHAASCVYLEELQKNGLSSEENMNASRMTLHR	480
Db	421	KTNIGKSSSSDLSKRPYIPDYKLAIEHHCFFHAASCVYLEELQKNGLSSEENMNASRMTLHR	480

OY	481	FGNSSSSSIWELAYMEAKESVRRGDYWOJAFSGGKCNVSYYWKARBYKKPPRNNPW	540
Dd	481	FGNSSSSSIWELAYMEAKESVRRGDYWOJAFDSGGKCNVSYYWKARBYKKPPRNNPW	540
OY	541	DCINRPVPL	550
Dd	541	DCINRPVPL	550

RESULT 4
Q9LLE5
ID Q9LLE5 PRELIMINARY; PRT; 550 AA

DT 01-OCT-2000 (TREMBlrel_15, Created)
DT 01-OCT-2000 (TREMBlrel_15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel_21, Last annotation update)
DE Fiddlehead protein.
GN Fdh.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20122614; PubMed=10655527;
RA Pruitt R.E., Vielle-Calzada J.P., Ploense S.E., Grossniklaus U.,
RA Lolle S.U.;
RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
RT in Arabidopsis, encodes a putative lipid biosynthetic enzyme.",
RL Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
DR EMBL; AF214502; AAF73979.1; -.
DR EMBL; AF214501; AAF73979.1; JOINED.
DR InterPro; IPR001099; N-C_synthase.
DR Pfam; PF02797; Chal_stil_synthc; 1.
DR ProDom; PD000453; N-C_synthase; 2.
SQ SEQUENCE 550 AA; 62606 MW; EDB7283601E64672 CRC64;

Query Match	99.78;	Score 2840;	DB 10;	Length 550;
Best Local Similarity	99.88;	Pred. No. 3.5e-227;		
Matches 549; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Oy	1	MGSNSEDOLLSTEIYNRRIEESGPNAGSPTESVYVRRLDPELOSVNKLKYGHLIN	60
Dd	1	MGRSBEOLLSTEIYNRRIEESGPNAGSPTESVYVRRLDPELOSVNKLKYGHLIN	60
Oy	61	HAVYLATIPVLVIVSAVGSLSREBIWKKLMDVDLATVIGFQGVFLTACVYMSRPS	120
Dd	61	HAVYLATIPVLVIVSAVGSLSREBIWKKLMDVDLATVIGFQGVFLTACVYMSRPS	120
Oy	121	YVLIDFACYKPSDEHKVTKEEFIELARKSGKFDEETIGFKRILIOASIGDETVPPSIS	180
Dd	121	YVLIDFACYKPSDEHKVTKEEFIELARKSGKFDEETIGFKRILIOASIGDETVPPSIS	180
Oy	181	SESENTTKKEEREPASVTYIFGALDELPEKTKYVKRKGVLVWNCSSINPPPSLAMYINH	240
Dd	181	SESENTTKKEEREPASVTYIFGALDELPEKTKYVKRKGVLVWNCSSINPPPSLAMYINH	240
Oy	241	YKMRGNILSYNLGGNGCSAGIIAIDLADMLOSPNSYAAVVSTEMYGNMYVGSDBKSMY	300
Dd	241	YKMRGNILSYNLGGNGCSAGIIAIDLADMLOSPNSYAAVVSTEMYGNMYVGSDBKSMY	300
Oy	301	IPNCFPRNGCSAVMLSNRRDPFRAKKTRLEIYVTHKAADDRSRSTYYOEDEDEGFGGLK	360
Dd	301	IPNCFPRNGCSAVMLSNRRDPFRAKKTRLEIYVTHKAADDRSRSTYYOEDEDEGFGGLK	360
Oy	361	ISRDLMEVGEALKTNTITTLGPVLVPSSEOLLFEPAALIRTFSPSAKTSSTTSPSTATA	420
Dd	361	ISRDLMEVGEALKTNTITTLGPVLVPSSEOLLFEPAALIRTFSPSAKTSSTTSPSTATA	420
Oy	421	KTNIGTKSSSOLSKRYPIDYKFLAEHFCFHAASRVVLELOKNIGLSEENNEASRMTLIHR	480
Dd	421	KTNIGTKSSSOLSKRYPIDYKFLAEHFCFHAASRVVLELOKNIGLSEENNEASRMTLIHR	480

OY 481 FGNSSSGIWEIAYMEAKESVRGRDVRWQIAGSGFKCNSVYKAMRKVKKPTRRNPV 540
 DB 481 FGNSSSGIWEIAYMEAKESVRGRDVRWQIAGSGFKCNSVYKAMRKVKKPTRRNPV 540
 OY 541 DCINRPVPL 550
 DB 541 DCINRPVPL 550

RESULT 5

OY 09LE6 PRELIMINARY; PRT; 508 AA.
 AC 09LE6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Fiddlehead protein.
 GN FDH.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-20122614; PubMed-10655527;
 RA Pruitt R.E., Vielle-Calzada J.P., Ploense S.E., Grossniklaus U.,
 RA Lolle S.J.;
 RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 in Arabidopsis, encodes a putative lipid biosynthetic enzyme.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
 DR EMBL; AF214500; AAF73978.1;
 DR EMBL; AF214499; AAF73978.1;
 DR InterPro: IPR001099; N-C-synthase.
 DR Pfam: PF02797; Chai_still_synthc; 1.
 DR Prodom: PD000453; N-C-synthase; 2.
 DR SEQUENCE 508 AA; 57043 MW; E034920567B0F96E CRC64;

Query Match 91.5%; Score 2605; DB 10; Length 508;
 Best Local Similarity 100.0%; Pred. No. 1e-207;
 Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGRNEDDLSTELVNRGIEPSGNAGSPTEVSRRRLPDLQSVNLKYLGYHYLIN 60
 DB 1 MGRNEDDLSTELVNRGIEPSGNAGSPTEVSRRRLPDLQSVNLKYLGYHYLIN 60
 OY 61 HAVYLAIPVLVLFSAEVSLSREELMKLMVDLAVIGFVFLTACVYFMSRPS 120
 DB 61 HAVYLAIPVLVLFSAEVSLSREELMKLMVDLAVIGFVFLTACVYFMSRPS 120
 OY 121 VYIDFACYRPSDEHKYTKKEEFILARKSGKFEDETLGFKKRIIQAAGIDETVPSRS 180
 DB 121 VYIDFACYRPSDEHKYTKKEEFILARKSGKFEDETLGFKKRIIQAAGIDETVPSRS 180
 OY 181 SSENITTMKEGREASTVIGALDELFEKTRVPRKDVGVLVNCSITNPPLISAMVINH 240
 DB 181 SSENITTMKEGREASTVIGALDELFEKTRVPRKDVGVLVNCSITNPPLISAMVINH 240
 OY 241 YKRGITLSTNLGMCSSAGIIAIDLRDLQSNPNSTAVYVSTEMGYWYVGSOSMY 300
 DB 241 YKRGITLSTNLGMCSSAGIIAIDLRDLQSNPNSTAVYVSTEMGYWYVGSOSMY 300
 OY 301 IPNCFRMCSSAVMLSNRRDRPHAKYRLHEHYTRHKAADRSFRSVYOEDEGFGKGLK 360
 DB 301 IPNCFRMCSSAVMLSNRRDRPHAKYRLHEHYTRHKAADRSFRSVYOEDEGFGKGLK 360
 OY 361 ISRDLMVEGALKNTITTLGPIVLPFSEDLFFALLRRTSPAKTSTTTSSTASARA 420
 DB 361 ISRDLMVEGALKNTITTLGPIVLPFSEDLFFALLRRTSPAKTSTTTSSTASARA 420
 OY 421 KTNIGKSSSDLSKPYIPDYKLAFEHFCFHAASKVYLELQKNLIGSEENMEASRMTLHR 480
 DB 421 KTNIGKSSSDLSKPYIPDYKLAFEHFCFHAASKVYLELQKNLIGSEENMEASRMTLHR 480

DB 421 KTNIGKSSSDLSKPYIPDYKLAFEHFCFHAASKVYLELQKNLIGSEENMEASRMTLHR 480
 OY 481 FGNSSSGIWEIAYMEAKESVRGRDVRWQIAGSGFKCNSVYKAMRKVKKPTRRNPV 540
 DB 481 FGNSSSGIWEIAYMEAKESVRGRDVRWQIAGSGFKCNSVYKAMRKVKKPTRRNPV 540

RESULT 6

OY 08VWP9 PRELIMINARY; PRT; 535 AA.
 AC 08VWP9;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Fiddlehead-like protein.
 GN FDH.
 OS Gossypium hirsutum (Upland cotton).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Gossypium.
 OX NCBI_Taxid=3635;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. XU-142; TISSUE-COTTON FIBER;
 RA Li C.-H., Zhu Y.-Q., Meng Y.-L., Wang J.-W., Xu K.-X., Zhang T.-Z.,
 RA Chen X.-Y.;
 RT "Isolation of Genes Preferentially Expressed in Cotton Fiber Cells by
 cDNA Array and RT-PCR."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY072823; AAL67993.1;
 DR InterPro: IPR001099; N-C-synthase.
 DR Pfam: PF02797; Chai_still_synthc; 1.
 DR Prodom: PD000453; N-C-synthase; 1.
 DR SEQUENCE 535 AA; 61123 MW; D3E8A8CEA7E1A6DE CRC64;

Query Match 81.6%; Score 2324; DB 10; Length 535;
 Best Local Similarity 80.1%; Pred. No. 2.4e-184;
 Matches 438; Conservative 48; Mismatches 41; Indels 20; Gaps 2;

OY 5 NEODLSTELVNRGIEPSGNAGSPTEVSRRRLPDLQSVNLKYLGYHYLINHAY 64
 DB 4 NEODLSTELVNRGIEPSGNAGSPTEVSRRRLPDLQSVNLKYLGYHYLINHAY 63
 OY 65 LATIPVLVLSAEVSLREELMKLM---YDLAVIGFGFVFLTACVYFMSRPSV 121
 DB 64 LATIPVLVLSAEVSLREELMKLMEDARYDLAVLSFAVFTVSVYFMSRPSI 123
 OY 122 YLIDFACYRPSDEHKYTKKEEFILARKSGKFEDETLGFKKRIIQAAGIDETVPSRS 181
 DB 124 YLIDFACYRPHDLAKTKDQFIELARASGKFEDETLGFKKRIIQAAGIDETVPSRS 183
 OY 182 SSENITTMKEGREASTVIGALDELFEKTRVPRKDVGVLVNCSITNPPLISAMVINH 241
 DB 184 KENCATMKEGRLASVTMFGALDELFEKTRIRKDVGLVNVCSITNPPLISAMVINH 243
 OY 242 KMGNTLSTNLGMCSSAGIIAIDLRDLQSNPNSTAVYVSTEMGYWYVGSOSMY 301
 DB 244 KMGNTLSTNLGMCSSAGIIAIDLRDLQSNPNSTAVYVSTEMGYWYVGSOSMY 303
 OY 302 PNCFFRMCSSAVMLSNRRDRPHAKYRLHEHYTRHKAADRSFRSVYOEDEGFGKGLK 361
 DB 304 PNCFFRMCSSAVMLSNRRDRPHAKYRLHEHYTRHKAADRSFRSVYOEDEGFGKGLK 363
 OY 362 SRDLMVEGALKNTITTLGPIVLPFSEDLFFALLRRTSPAKTSTTTSSTASARA 421
 DB 364 SKDITLIGGDAKNTITTLGPIVLPFSEDLFFALLRRTSPAKTSTTTSSTASARA 420
 OY 422 TNGIKSSSDLSKPYIPDYKLAFEHFCFHAASKVYLELQKNLIGSEENMEASRMTLHR 481
 DB 411 ----TSLSPSSKPYIPDYKLAFEHFCFHAASKVYLELQKNLIGSEENMEASRMTLHR 466
 OY 482 GNTSSSGIWEIAYMEAKESVRGRDVRWQIAGSGFKCNSVYKAMRKVKKPTRRNPV 541
 DB 482 GNTSSSGIWEIAYMEAKESVRGRDVRWQIAGSGFKCNSVYKAMRKVKKPTRRNPV 541

Db 467 GNTSSSIWEIAYLEAKERYKRGDRIMQIAFGSGFKNSVYVMSRMRYRKPDRPNMUD 526
QY 542 CINTRPV 548
Db 527 CIDRYPV 533

RESULT 7

0852R3 PRELIMINARY; PRT; 526 AA.
AC 0852R3;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative beta-ketoacyl-CoA synthase.
GN APT.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Veroniceae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RA Yephremov A., Efremova N., Heidmann I., Huijser P., Wellesen K.,
RA Schwarz-Sommer Z., Saedler H.;
RT "Epidermis-specific expression of FIDDLEHEAD-like genes in Arabidopsis
RT and Antirrhinum";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ310739; CAC84082.1;
SQ SEQUENCE 526 AA; 59277 MW; 43247EA83B257444 CRC64;

Query Match 76.4%; Score 2175.5; DB 10; Length 526;
Best Local Similarity 74.8%; Pred. No. 5e-172;
Matches 410; Conservative 60; Mismatches 47; Indels 31; Gaps 4;

QY 4 SNEODLSTELIYNRGIEPSGPNAGSPTEFSVRRRLPDLQSYNLKYYKLGHYLYLNHAY 63
Db 2 ASEQMLSTELIYNRGIE-----AGAMTFSVRRRLPDLQSYNLKYYKLGHYLYLNHGI 56
QY 64 YLATIPVLYVLSAEVGSLSREIWKKLM-----YDLATVIGFGVFLVLTACYFMSRPR 119
Db 57 YLATIPVLYVLSAEVGSLSREIWKKLM-----YDLATVIGFGVFLVLTACYFMSRPR 116
QY 120 SVYLDIFACYPSPDEHKYTKKEEFIELARKSGKDEETLGFKRRILOASIGDETVPRSI 179
Db 117 SYIYLDIFACYPSPDLKTKKEEFIELARKSGKFTESSEFKRRILOASIGDETVPRSI 176
QY 180 SSENITTMKEGREGASTVIFGALDELFEKTRVYKPKDGVLYVNCISFNPTPSLSAMVIN 239
Db 177 ASSENTATMKREGTEASTVIFGALDELFEKTHIRPKDGVLYVNCISFNPTPSLSAMVIN 236
QY 240 HYKMGNTLSYNGMGCSAGIATIDLARMLQSNPNSAVVYSTEVMGYNNYVSDSKM 299
Db 237 HYKMGNTLSYNGMGCSAGIATIDLARMLQSNPNSAVVYSTEVMGYNNYVSDSKM 296
QY 300 VIPNCFPMGCSAVMLSNRRDRFRAKYRLEHIVRTHKAADRSFRSVYQEDDQGFGLK 359
Db 297 LIPNCFPMGCSAVMLSNRRDRYGAAYRLEHIVRTHKAGADRSFRSVYQEDDQGFGLK 356
QY 360 KISRLMEVGEALTKNTITTLGVLVLPFSEQLFFAALLRTFSPAARTSTTSTSTAT 419
Db 357 KYSKDLVEIGEAIRKNTITTLGVLVLPFSEQLFFSTLVMKLSGSGANSMS----- 408
QY 420 AKTNGIKSSSSDLSPYIPDYKLAFEHFCFAASKVYLELOKNGKLGSENNKASMTLH 479
Db 409 -----SNPYIPDYKLAFEHFCMAASKVYLELOKNGKLGSENNKASMTLH 455
QY 480 REGNTSSGIWEIAYLEAKERYKRGDRIMQIAFGSGFKNSVYVMSRMRYRKPDRPNMUD 539
Db 456 REGNTSSSIWEIAYLEAKERYKRGDRIMQIAFGSGFKNSVYVMSRMRYRKPDRPNMUD 514
QY 540 VDCINRYP 547
Db 527 CIDRYPV 533

Db 515 VDCIDGYP 522

RESULT 8

09LE7 PRELIMINARY; PRT; 389 AA.
AC 09LE7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 21, Last annotation update)
DE Fiddlehead protein.
GN FDH.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eustoidia II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20122614; PubMed=10655527;
RA Pruitt R.E., Viatte-Calzada J.P., Ploense S.E., Grossniklaus U.,
RA Lohle S.J.;
RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
RT in Arabidopsis, encodes a putative lipid biosynthetic enzyme.";
RT Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
DR EMBL; AF214498; AAF73977.1;
DR EMBL; AF214497; AAF73977.1; JOINED.
DR InterPro; IPR001099; N-C_synthase.
DR ProDom; PD000453; N-C_synthase; 1.
SQ SEQUENCE 389 AA; 43765 MW; 3F305FA5F8AE7523 CRC64;

Query Match 70.4%; Score 2005; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 4.6e-158;
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSNEODLSTELIYNRGIEPSGPNAGSPTEFSVRRRLPDLQSYNLKYYKLGHYLYLNHAY 60
Db 1 MGRSNEODLSTELIYNRGIEPSGPNAGSPTEFSVRRRLPDLQSYNLKYYKLGHYLYLNHGI 60
QY 61 HAVYIATIPVLYVLSAEVGSLSREIWKKLMYDYLATVIGFGVFLVLTACYFMSRPRS 120
Db 61 HAVYIATIPVLYVLSAEVGSLSREIWKKLMYDYLATVIGFGVFLVLTACYFMSRPRS 120
QY 121 VYLIDPACYPSPDEHKYTKKEEFIELARKSGKDEETLGFKRRILOASIGDETVPRSI 180
Db 121 VYLIDPACYPSPDEHKYTKKEEFIELARKSGKDEETLGFKRRILOASIGDETVPRSI 180
QY 181 SSENITTMKEGREGASTVIFGALDELFEKTRVYKPKDGVLYVNCISFNPTPSLSAMVIN 240
Db 181 SSENITTMKEGREGASTVIFGALDELFEKTRVYKPKDGVLYVNCISFNPTPSLSAMVIN 240
QY 241 YKMGNTLSYNGMGCSAGIATIDLARMLQSNPNSAVVYSTEVMGYNNYVSDSKM 300
Db 241 YKMGNTLSYNGMGCSAGIATIDLARMLQSNPNSAVVYSTEVMGYNNYVSDSKM 300
QY 301 IPNCFPMGCSAVMLSNRRDRFRAKYRLEHIVRTHKAADRSFRSVYQEDDQGFGLK 360
Db 301 IPNCFPMGCSAVMLSNRRDRFRAKYRLEHIVRTHKAADRSFRSVYQEDDQGFGLK 360
QY 361 ISRLMEVGEALTKNTITTLGVLVLPFSE 389
Db 361 ISRLMEVGEALTKNTITTLGVLVLPFSE 389
RESULT 9
09LE3 PRELIMINARY; PRT; 352 AA.
AC 09LE3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 21, Last annotation update)
DE Fiddlehead protein.
GN FDH.

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;
 RX SEQUENCE FROM N.A.
 RA MEDLINE-20122614; PubMed-10655527;
 RA Pruitt R.E., Velle-Calzada J.P., Ploense S.E., Grossniklaus U.,
 RA Lolle S.J.;
 RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 RT in Arabidopsis, encodes a putative lipid biosynthetic enzyme.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
 DR EMBL: AF214505; AAF73981.1; JOINED.
 DR InterPro: IPR001099; N-C-synthase.
 DR ProDom: PD000453; N-C-synthase; 1.
 SQ SEQUENCE 352 AA; 39793 MW; D31A8B2396E286E CRC64;

Query Match 63.9%; Score 1820; DB 10; Length 352;
 Best Local Similarity 100.0%; Pred. No. 9.1e-143;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSNEODLLSTEIVNRGIEPSPGNAGSPFESVRVRRLPDPFLOSVMKYGHYLN 60
 DB 1 MGRSNEODLLSTEIVNRGIEPSPGNAGSPFESVRVRRLPDPFLOSVMKYGHYLN 60
 QY 61 HAVYATIPVLVLFSAEVSLSREIWKLMYDLYATVIGFGVFLVACVYFMSRPRS 120
 DB 61 HAVYATIPVLVLFSAEVSLSREIWKLMYDLYATVIGFGVFLVACVYFMSRPRS 120
 QY 121 VYLIDFACYPDEHKVYKEEFTELARKSGKFEDETLGFKRRLQASGIGDETYVPRSS 180
 DB 121 VYLIDFACYPDEHKVYKEEFTELARKSGKFEDETLGFKRRLQASGIGDETYVPRSS 180
 QY 181 SSENTITMKEGREASTVIFGALDELFEKTRVYKPKDVGVLVNCSTFNPPLSAMVINH 240
 DB 181 SSENTITMKEGREASTVIFGALDELFEKTRVYKPKDVGVLVNCSTFNPPLSAMVINH 240
 QY 241 YKMRGNILSYNGMGCSAGIITDARDMLQSNPNYSYAVVSTEMVGYNMVYSGDSKSV 300
 DB 241 YKMRGNILSYNGMGCSAGIITDARDMLQSNPNYSYAVVSTEMVGYNMVYSGDSKSV 300
 QY 301 IPNCFPRMGCSAVMLSNRRDRFRAKYRLEHIVRTHKADDRSFR 352
 DB 301 IPNCFPRMGCSAVMLSNRRDRFRAKYRLEHIVRTHKADDRSFR 352

RESULT 10

Q9LNDX6 PRELIMINARY; PRT; 351 AA.
 AC Q9LNDX6;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Fiddlehead protein.
 GN FHL.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;
 RX SEQUENCE FROM N.A.
 RA MEDLINE-20122614; PubMed-10655527;
 RA Pruitt R.E., Velle-Calzada J.P., Ploense S.E., Grossniklaus U.,
 RA Lolle S.J.;
 RT "FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 RT in Arabidopsis, encodes a putative lipid biosynthetic enzyme.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1311-1316(2000).
 DR EMBL: AF214494; AAF73975.1; JOINED.
 DR EMBL: AF214493; AAF73975.1; JOINED.
 DR EMBL: AF214492; AAF73974.1; JOINED.

DR EMBL: AF214491; AAF73974.1; JOINED.
 DR InterPro: IPR001099; N-C-synthase.
 DR ProDom: PD000453; N-C-synthase; 1.
 SQ SEQUENCE 351 AA; 39810 MW; 41F0CD279D141EC8 CRC64;

Query Match 62.6%; Score 1784; DB 10; Length 351;
 Best Local Similarity 100.0%; Pred. No. 8.9e-140;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSNEODLLSTEIVNRGIEPSPGNAGSPFESVRVRRLPDPFLOSVMKYGHYLN 60
 DB 1 MGRSNEODLLSTEIVNRGIEPSPGNAGSPFESVRVRRLPDPFLOSVMKYGHYLN 60
 QY 61 HAVYATIPVLVLFSAEVSLSREIWKLMYDLYATVIGFGVFLVACVYFMSRPRS 120
 DB 61 HAVYATIPVLVLFSAEVSLSREIWKLMYDLYATVIGFGVFLVACVYFMSRPRS 120
 QY 121 VYLIDFACYPDEHKVYKEEFTELARKSGKFEDETLGFKRRLQASGIGDETYVPRSS 180
 DB 121 VYLIDFACYPDEHKVYKEEFTELARKSGKFEDETLGFKRRLQASGIGDETYVPRSS 180
 QY 181 SSENTITMKEGREASTVIFGALDELFEKTRVYKPKDVGVLVNCSTFNPPLSAMVINH 240
 DB 181 SSENTITMKEGREASTVIFGALDELFEKTRVYKPKDVGVLVNCSTFNPPLSAMVINH 240
 QY 241 YKMRGNILSYNGMGCSAGIITDARDMLQSNPNYSYAVVSTEMVGYNMVYSGDSKSV 300
 DB 241 YKMRGNILSYNGMGCSAGIITDARDMLQSNPNYSYAVVSTEMVGYNMVYSGDSKSV 300
 QY 301 IPNCFPRMGCSAVMLSNRRDRFRAKYRLEHIVRTHKADDRSFR 345
 DB 301 IPNCFPRMGCSAVMLSNRRDRFRAKYRLEHIVRTHKADDRSFR 345

RESULT 11

Q9LND49 PRELIMINARY; PRT; 516 AA.
 AC Q9LND49;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE F18014.21.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;
 RX SEQUENCE FROM N.A.
 RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
 RA Kim C., Altafi H., Bel O., Chin C., Chlou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thavert A.,
 RA Toriumi M., Vayberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC F18014 from chromosome
 RT 1.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC025808; AAF79428.1; JOINED.
 DR InterPro: IPR001099; N-C-synthase.
 DR Pfam: PF02797; Chal-st1L_synth; 1.
 DR ProDom: PD000453; N-C-synthase; 1.
 SQ SEQUENCE 516 AA; 57842 MW; 3EDD488EE755C367 CRC64;

Query Match 55.1%; Score 1569; DB 10; Length 516;
 Best Local Similarity 56.5%; Pred. No. 1.2e-121;
 Matches 300; Conservative 82; Mismatches 117; Indels 32; Gaps 5;

QY 23 GPNAGSPFESVRVRRLPDPFLOSVMKYGHYLNHAVYATIPVLVLFSAEVSLS 82
 DB 13 GGGDGSVGVQIRGTALPDPFLOSVMKYGHYLNILTLCLFP-LAVYATSEASOM 71

RESULT	14			
09FXZ8				
ID	09FXZ8	PRELIMINARY;	PRT;	513 AA.
AC	09FXZ8;			
DT	01-MAR-2001 (TREMBlrel. 16, Created)			
DT	01-MAR-2001 (TREMBlrel. 16, Last sequence update)			
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
DE	Putative fatty acid elongase.			
GN	FAR2.			
OS	Zea mays (Maize).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Lillipsoida; Poales; Poaceae; PACC clade.			
OC	Panicoidae; Andropogoneae; Zea.			
OX	NCBI_TaxID=4577;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=21116804; PubMed=11171156;			
RX	Schreiber L., Skrabs M., Hartmann K., Becker D., Cassagne C.,			
RA	Leslie R.;			
RT	"Biochemical and molecular characterisation of corn (Zea mays L.) root			
RT	elongases.";			
RT	Biochem. Soc. Trans. 28:647-649(2000).			
RL	EMBL: AJ929770; CAC01441.1; "			
DR	InterPro: IPR001099; N-C-synthase.			

SEQUENCE	505 AA.	PRT;	PRELIMINARY;	09FEV67	RESULT 15
SO	SEQUENCE 505 AA.; 56549 MW; EFCA1BAD807B0AB6 CRC64;				
DR	Prodom: PF000453; N-C-synthase; 1.				
DR	InterPro: IPR001099; N-C-synthase.				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	soybean embryos."				
DR	"Production of fatty acid components of meadowfoam oil in somatic				
DR	soybean embryos."				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	InterPro: IPR001099; N-C-synthase.				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	soybean embryos."				
DR	"Production of fatty acid components of meadowfoam oil in somatic				
DR	soybean embryos."				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	InterPro: IPR001099; N-C-synthase.				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	soybean embryos."				
DR	"Production of fatty acid components of meadowfoam oil in somatic				
DR	soybean embryos."				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	InterPro: IPR001099; N-C-synthase.				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	soybean embryos."				
DR	"Production of fatty acid components of meadowfoam oil in somatic				
DR	soybean embryos."				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	InterPro: IPR001099; N-C-synthase.				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	soybean embryos."				
DR	"Production of fatty acid components of meadowfoam oil in somatic				
DR	soybean embryos."				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	InterPro: IPR001099; N-C-synthase.				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	soybean embryos."				
DR	"Production of fatty acid components of meadowfoam oil in somatic				
DR	soybean embryos."				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	InterPro: IPR001099; N-C-synthase.				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	soybean embryos."				
DR	"Production of fatty acid components of meadowfoam oil in somatic				
DR	soybean embryos."				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	InterPro: IPR001099; N-C-synthase.				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	soybean embryos."				
DR	"Production of fatty acid components of meadowfoam oil in somatic				
DR	soybean embryos."				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	InterPro: IPR001099; N-C-synthase.				
DR	Plant Physiol. 124:243-253(2000).				
DR	EMBL: AF247134; AAC286500.1; "				
DR	soybean embryos."				
DR	"Production of fatty acid components of meadowfoam oil in somatic				
DR	soybean embryos."				
DR	Plant Physiol. 124:2				

Query Match 51.6%; Score 1470.5; DB 10; Length 505;
 Best Local Similarity 52.5%; Pred. No. 1,7e-113;
 Matches 272; Conservative 100; Mismatches 113; Indels 33; Gaps 5;

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QY 35 VRRRLPDLQSVNLKYYKLGHYHLINHAVALATIPVLVFSAEVGSLSRE--EIMWKL 91
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Db 14 VKNTLPDLKLSINKHVKLGHYHLITHGMYLC-LPPLALVYFAQISTLSLKDNDIMEQL 72
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 92 WDDDLAVIFGFGVYLTACYFMSRPSRYLLIDFACYSDEHKVTKKEPIELARKSGK 151
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 73 -QENLSVYVSTLVSLLLYEFTRPYPYLMDFACYKPDETRSTREHEMKCESLSGS 131
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 152 FDEETLGFKKRILOAGIGDETVYPRSSISENTTMMKEGREASTYIFGALDELEFEKTR 211
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 132 FTEENIDFQKLVARSGLGDTYLPDAIGTIPAHPSMAARREBELVFGAIDQLEKTK 191
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 212 VKPRDGVLVVNCISIFNPTPSLSAMVINHYKMRGNILSYNLGMCAGIATIDLARDML 271
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 192 VNPRDIGILVYVNCISLFPPTPSLSMIVNHKRLRGNITISYNLGMCAGISVDLAKRL 251
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 272 QSNPNSTAAVYVSTEMVGYNNYVGSDKSMVLPNCFRMCSSAVMLSNRRRDFRHAQYRL 331
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 252 ETNPNITVALWSTENTILNMYMGNDRSKLVNCLFRMGGAAYLLSNKTSDKRSKYQLVT 311
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QY 332 IVRTKAADDRSFERSYVQEEDGQFGKLGKISRDLMVEYGEALKTNTITLGPVLVPSFQL 391
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 312 TVRSHKAGADNCGICIQEEDSNCKIGVSLSKNLMAVAGDALKTNTITLGPVLVPMSEQL 371
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 392 LFPFALL-RRTFSPAATSTTTSFSTGATKNGIKSSSDLSKPYIPDYKILAEHFCH 450
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 372 LFEATLVARRKVFKKI-----KPYIPDFKLAFDHCIH 404
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 451 AASVYVLEELQKNGISENNMEASRMTLHFRGNTSSSGIWEYELAYMEAKESVRGRDRWQ 510
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 405 AGGAVALDELEKLNQSSMHLBPSRMTLYRGRNTSSSSLMWEIAYSEAKGRIRGERVWQ 464
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 511 IAFSGGFCNSVYKAKRKYKKPTRRNPWVDCINRYPV 548
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 465 IGFSGGFCNSAVWKAALKSYDPKKERKPNWDEIHQFPV 502
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OM protein - protein search, using sw model

Run on: May 10, 2003, 23:50:32 ; Search time 613 Seconds
(without alignments)
82.568 Million cell updates/sec

Title: US-09-905-657-2

Perfect score: 2848
Sequence: 1 MGRSNEQDLSTEIVNRGIE.....KKPTRNPWVCINRPVPL 550

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2848	100.0	550	10	US-09-905-657-2 Sequence 2, Appl 1
2	2845	99.9	550	10	US-09-883-797-8 Sequence 8, Appl 1
3	1569	55.1	516	10	US-09-883-797-14 Sequence 14, Appl 1
4	1493	52.4	537	10	US-09-883-797-10 Sequence 10, Appl 1
5	1446.5	50.8	500	10	US-09-883-797-12 Sequence 12, Appl 1
6	1445	50.7	497	10	US-09-892-325-4 Sequence 4, Appl 1
7	1438	50.5	520	10	US-09-883-797-2 Sequence 2, Appl 1
8	1200	42.1	506	10	US-09-877-476-42 Sequence 42, Appl 1
9	1197.5	42.0	505	10	US-09-877-476-6 Sequence 6, Appl 1
10	1194	41.9	493	10	US-09-883-797-4 Sequence 4, Appl 1
11	1193	41.9	506	10	US-09-877-476-32 Sequence 32, Appl 1
12	1190	41.8	506	10	US-09-877-476-38 Sequence 38, Appl 1
13	1190	41.8	506	10	US-09-877-476-40 Sequence 40, Appl 1
14	1187	41.7	506	10	US-09-877-476-34 Sequence 34, Appl 1
15	1186	41.6	506	10	US-09-877-476-2 Sequence 2, Appl 1
16	1186	41.6	506	10	US-09-877-476-16 Sequence 16, Appl 1
17	1183	41.5	506	10	US-09-877-476-22 Sequence 22, Appl 1
18	1183	41.5	506	10	US-09-877-476-26 Sequence 26, Appl 1
19	1183	41.5	506	10	US-09-877-476-36 Sequence 36, Appl 1

20	1182	41.5	506	10	US-09-877-476-24 Sequence 24, Appl 1
21	1181	41.5	506	10	US-09-877-476-20 Sequence 20, Appl 1
22	1180	41.4	506	10	US-09-877-476-4 Sequence 4, Appl 1
23	1179	41.4	506	10	US-09-877-476-28 Sequence 28, Appl 1
24	1176	41.3	506	10	US-09-877-476-14 Sequence 14, Appl 1
25	1175	41.3	506	10	US-09-877-476-8 Sequence 8, Appl 1
26	1174	41.2	506	10	US-09-877-476-12 Sequence 12, Appl 1
27	1173	41.2	506	10	US-09-877-476-30 Sequence 30, Appl 1
28	1172.5	41.2	505	10	US-09-877-476-18 Sequence 18, Appl 1
29	1170.5	41.1	504	10	US-09-883-797-6 Sequence 6, Appl 1
30	1165.5	40.9	505	10	US-09-877-476-10 Sequence 10, Appl 1
31	156	5.5	351	9	US-09-829-378-5 Sequence 5, Appl 1
32	148.5	5.2	83	10	US-09-903-456-8 Sequence 8, Appl 1
33	145	5.1	317	10	US-09-815-242-14037 Sequence 14037, A
34	141	5.0	317	10	US-09-815-242-10124 Sequence 10124, A
35	131.5	4.6	313	10	US-09-815-242-12528 Sequence 12528, A
36	127.5	4.5	360	9	US-09-829-378-3 Sequence 3, Appl 1
37	125.5	4.4	394	10	US-09-837-654-1 Sequence 1, Appl 1
38	125.5	4.4	394	10	US-09-837-554-1 Sequence 1, Appl 1
39	122	4.3	331	10	US-09-815-242-11484 Sequence 11484, A
40	122	4.3	360	9	US-09-829-378-4 Sequence 4, Appl 1
41	117	4.1	316	10	US-09-815-242-10976 Sequence 10976, A
42	115.5	4.1	744	9	US-10-270-875-12 Sequence 12, Appl 1
43	115.5	4.1	744	9	US-10-270-878-12 Sequence 12, Appl 1
44	107	3.8	412	9	US-09-829-378-2 Sequence 2, Appl 1
45	102.5	3.6	360	9	US-09-829-378-6 Sequence 6, Appl 1

ALIGNMENTS

RESULT 1

US-09-905-657-2
Sequence 2, Application US/09905657
Patent No. US20020038471A1
GENERAL INFORMATION:
APPLICANT: BAYER AG
TITLE OF INVENTION: Use of VICEF for identifying herbicidally
FILE REFERENCE: Le A 34 730
CURRENT APPLICATION NUMBER: US/09/905,657
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 550
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-905-657-2

Query Match	100.0%	Score 2848;	DB 10;	Length 550;
Best Local Similarity	100.0%	Pred. No. 3.3e-236;		
Matches 550;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1	MGRSNEQDLSTEIVNRGIEPSGPNAGSPTFSVRRRLPDFLOSYNLKYKLGHYLIN	60	
DB	1	MGRSNEQDLSTEIVNRGIEPSGPNAGSPTFSVRRRLPDFLOSYNLKYKLGHYLIN	60	
OY	61	HAVYATATPVLVFAEYSGLSREIEIMKLMYDIATVIGFVFLTACVYFMSRPS	120	
DB	61	HAVYATATPVLVFAEYSGLSREIEIMKLMYDIATVIGFVFLTACVYFMSRPS	120	
OY	121	VYLIDPACRPSDEHVTVEEFTELARKSGKDEETLGKRRILQASGIGDEYVRSIS	180	
DB	121	VYLIDPACRPSDEHVTVEEFTELARKSGKDEETLGKRRILQASGIGDEYVRSIS	180	
OY	181	SENTITMKEGREASTVFGALDELFEKTRVPRKVGVLVVNCSTFNPPTSANVINH	240	
DB	181	SENTITMKEGREASTVFGALDELFEKTRVPRKVGVLVVNCSTFNPPTSANVINH	240	
OY	241	YKRGNIISYNIGCMCSAGIATIDARDMLQSNPNSYAVVSTEWGYGNWYGSQSMV	300	
DB	241	YKRGNIISYNIGCMCSAGIATIDARDMLQSNPNSYAVVSTEWGYGNWYGSQSMV	300	

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QY 301 IPNCFRMCSSAVMLSNRRDPRHAKYRLHEIVTRHKAADRSPRSYQOEDEQFGKGLK 360
Db 301 IPNCFRMCSSAVMLSNRRDPRHAKYRLHEIVTRHKAADRSPRSYQOEDEQFGKGLK 360
QY 361 ISDLMVEVGEALKTNTITLGPVLVPSSEQLLFFAALVTRTFSPAATSTTTSFSTATA 420
Db 361 ISDLMVEVGEALKTNTITLGPVLVPSSEQLLFFAALVTRTFSPAATSTTTSFSTATA 420
QY 421 KTGKIKSSSDLSKPYIPDKLAFEHFCFHAASKVYLEEOKNLGISEENMEASRMTLHR 480
Db 421 KTGKIKSSSDLSKPYIPDKLAFEHFCFHAASKVYLEEOKNLGISEENMEASRMTLHR 480
QY 481 FGMTSSGIVELAYLWAKESVRRGDRVWQIAFGSGFKCNVYWKAMRYKKPTRNPNW 540
Db 481 FGMTSSGIVELAYLWAKESVRRGDRVWQIAFGSGFKCNVYWKAMRYKKPTRNPNW 540
QY 541 DCINRYPVPL 550
Db 541 DCINRYPVPL 550

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RESULT 2
US-09-883-797-8
; Sequence 8, Application US/09883797
; Patent No. US20020066123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemmiller, Martha A.
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-883-797-8

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Query Match          99.98; Score 2845; DB 10; Length 550;
Best Local Similarity 99.88; Pred. No. 6.4e-256;
Matches 549; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGRSNEODLLSTELVNRGIEPSGPNAGSPRPSVVRRLPDQLQSVNLKYKLGHYHLIN 60
Db 1 MGRSNEODLLSTELVNRGIEPSGPNAGSPRPSVVRRLPDQLQSVNLKYKLGHYHLIN 60
QY 61 HAYLATIPLVLYFSAEVSLSREETIMKLMYDLATVIGFVFLTACVYFMSRPRS 120
Db 61 HAYLATIPLVLYFSAEVSLSREETIMKLMYDLATVIGFVFLTACVYFMSRPRS 120
QY 121 VYLIDFACYPSDEHKYTKKEETELAKRSKGFDEETGFKRILQASGIDETVPPRSIS 180
Db 121 VYLIDFACYPSDEHKYTKKEETELAKRSKGFDEETGFKRILQASGIDETVPPRSIS 180
QY 181 SSENITTMKREGEASTVIGALDELFEKTRVPRKDVGVVNCSTINPPTPSLAWYIN 240
Db 181 SSENITTMKREGEASTVIGALDELFEKTRVPRKDVGVVNCSTINPPTPSLAWYIN 240
QY 241 YKRGITLSTNLGMCSSAGIIDLARDMLQSNPNSYAVVSTEMYGVWYVGSOKSMV 300
Db 241 YKRGITLSTNLGMCSSAGIIDLARDMLQSNPNSYAVVSTEMYGVWYVGSOKSMV 300
QY 301 IPNCFRMCSSAVMLSNRRDPRHAKYRLHEIVTRHKAADRSPRSYQOEDEQFGKGLK 360
Db 301 IPNCFRMCSSAVMLSNRRDPRHAKYRLHEIVTRHKAADRSPRSYQOEDEQFGKGLK 360
QY 361 ISDLMVEVGEALKTNTITLGPVLVPSSEQLLFFAALVTRTFSPAATSTTTSFSTATA 420

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Db 361 ISDLMVEVGEALKTNTITLGPVLVPSSEQLLFFAALVTRTFSPAATSTTTSFSTATA 420
QY 421 KTGKIKSSSDLSKPYIPDKLAFEHFCFHAASKVYLEEOKNLGISEENMEASRMTLHR 480
Db 421 KTGKIKSSSDLSKPYIPDKLAFEHFCFHAASKVYLEEOKNLGISEENMEASRMTLHR 480
QY 481 FGMTSSGIVELAYLWAKESVRRGDRVWQIAFGSGFKCNVYWKAMRYKKPTRNPNW 540
Db 481 FGMTSSGIVELAYLWAKESVRRGDRVWQIAFGSGFKCNVYWKAMRYKKPTRNPNW 540
QY 541 DCINRYPVPL 550
Db 541 DCINRYPVPL 550

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RESULT 3
US-09-883-797-14
; Sequence 14, Application US/09883797
; Patent No. US20020066123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemmiller, Martha A.
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-883-797-14

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Query Match          55.18; Score 1569; DB 10; Length 516;
Best Local Similarity 56.58; Pred. No. 2.6e-137;
Matches 300; Conservative 82; Mismatches 117; Indels 32; Gaps 5;
QY 23 GPNAGSPRPSVVRRLPDQLQSVNLKYKLGHYHLINHAYLATIPLVLYFSAEVSLS 82
Db 13 GGGGDSVGVQIRQIRMLDQLQSVNLKYKLGHYHLINLTLCLFP-LAVIVISVSAQ 71
QY 83 SREIETIMKLM--DYDLATVIGFVFLTACVYFMSRPRSIVLIDFACYPSDEHKYTK 139
Db 72 NPDDL-KQLMIHLQNLVSIILCSALVFGLTVMRPRVYLVDSCLIPPHILAPY 130
QY 140 EEFTELAKRSKGFDEETGFKRILQASGIDETVPPRSISSSENITTMKREGEASTVI 199
Db 131 ARFESHRLTGDQDLSALEFQKILERSGLDEDTYVEAMHYVPRISMAAREADQVM 190
QY 200 FGALDELFEKTRVPRKDVGVVNCSTINPPTPSLAWYINHYKRGITLSTNLGMCSSA 259
Db 191 FGALDNLFANTINVKRIGILVNCSTINPPTPSLAWYINHYKRGITLSTNLGMCSSA 250
QY 260 GIATIDLARDMLQSNPNSYAVVSTEMYGVWYVGSOKSMVIPNCFRMCSSAVMLSNRR 319
Db 251 GVALVDAKMDLVHRTYAVVSTEMIYNWFGNKKSMILRNCLEFRVGSVAVLSNKS 310
QY 320 RDRHAKYRLHEIVTRHKAADRSPRSYQOEDEQFGKGLKISDLMVEVGEALKTNTIT 379
Db 311 RDRRSKRYRLVHVRHGRGADDAFRVYQEOODTGRTVSLKDLALINGELTKNTIT 370
QY 380 LGPVLVPSSEQLLFFAALVTRTFSPAATSTTTSFSTATAKTNGIKSSSDLSKPYIPD 439
Db 371 LGPVLVPSSEQLLFFAALVTRTFSPAATSTTTSFSTATAKTNGIKSSSDLSKPYIPD 404
QY 440 YKLAFEHFCFHAASKVYLEEOKNLGISEENMEASRMTLHRFGNTSSGIVELAYLWAK 499
Db 405 YKLAFEHFCFHAASKVYLEEOKNLGISEENMEASRMTLHRFGNTSSGIVELAYLWAK 464

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OY 500 ESVRGRVMOIARSGFKNSVYKARKYKPTNNPWDCINRYVPL 550
Db 465 GRMRGRNVMQIARSGFKNSAIWEALRHV-KPSNNSPWDCIDKYPVTL 514

RESULT 4
US-09-883-797-10

; Sequence 10, Application US/09883797
; Patent No. US2002006123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 537
; TYPE: PR1
; ORGANISM: Arabidopsis thaliana
US-09-883-797-10

Query Match

Best Local Similarity 52.4%; Score 1493; DB 10; Length 537;
Matches 287; Conservative 103; Mismatches 116; Indels 40; Gaps 9;

OY 12 TEIYNRGIEBSPNAGSPTSVRV---RRRLPDLQSVNLTAKYKLGHYHINHAVALYAT 67
Db 23 SEAEANEP--VNGS--VOIRTEENRRRLPDLQSVNLTAKYKLGHYHINHAVALYAT 78
OY 68 IPVLVLSAEVSLSREIKKTL--DYDLATVIGFVGLTACVYEMSRPSVYLI 124
Db 79 VP-LMAVLVEISRLTDDLT-QIMLQIYNLVAFILSALATIGSTYIMSRPSVYLV 136
OY 125 DFACVPSDEHKTKEEFIELARKSGDETLGFKRILOASGIDETVYPRSSSEN 184
Db 137 DYSCLPESLOVYKQFMDSKLIEDENESSLEFORKILERSGIDETVYPRALHCP 196
OY 185 ITTKEGREASTYIFGALDELFEKTRKPKDGVLYVNCISFNTPSLAMVINHYMR 244
Db 197 RPTMAARESEOVYMFGLDKLFENTKINPRDIGLVVNCISFNTPSLAMVINHYMR 256
OY 245 GNLSYNLGSGSAGIATDILARDMLQSNPSYAVVSTWVGWVGSDDKSVIPNC 304
Db 257 GNVSPNLGSGSAGIATDILARDMLQSNPSYAVVSTWVGWVGSDDKSVIPNC 316
OY 305 FFMGCSAVMLSNRRDFRRAKRYLEHIVTHKAADRSFRSVYQEEDEOGFKLISRD 364
Db 317 LFRVGSAILLSNKGDRRSKRYLVHTVTHKGAVERKAFNCVQEOEDNGKTVGSLKD 376
OY 365 LMEVGEALKTNTTLPVLPSEQLFPALALRRTSPAAKTSTTTSFSTATAKING 424
Db 377 LMAIAGEALKNTTTLGLVLPISQILFEMTIVTK----- 412
OY 425 IKSSSDLSKRYIPDYKLAFFHCFEHAASKVYLELOKNLGLSEENMEASRMTLHRFGNT 484
Db 413 -KLENSKL-KRYPDFKLAFFHCFHAGRAVIDELEKNLQSHVASSRMTLHRFGNT 470
OY 485 SSSGIWEELAYMEAKESVGRVMOIARSGFKNSVYKARKYKPTNNPWDCIN 544
Db 471 SSSSIWEELAYIEAKGRKGRNVMQIARSGFKNSAVVALLNV-KPSVSSPHECID 529
OY 545 RYVPL 550
Db 530 RYVPL 535

RESULT 5
US-09-883-797-12

; Sequence 12, Application US/09883797
; Patent No. US2002006123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 500
; TYPE: PR1
; ORGANISM: Arabidopsis thaliana
US-09-883-797-12

Query Match

Best Local Similarity 50.8%; Score 1446.5; DB 10; Length 500;
Matches 281; Conservative 94; Mismatches 111; Indels 41; Gaps 9;

OY 28 SPTSVRRRLPDLQSVNLTAKYKLGHYHINHAVALYATPVLYVLSAEVSLSREI 87
Db 1 SPTVP---QAMPPESSSVKLYKLGHYHINHAVALYATPVLYVLSAEVSLSREI 56
OY 88 ---WKKLMDYLAIV--GFGVFLTACVYEMSRPSVYLIIDFACVPSDEHKTKEEF 142
Db 57 LNMVSL-QPDLVOYLCSSFEVIFST--VFMSPRTIYLDVDSCTVPTCTRPATP 113
OY 143 IELARKSGPDETLGFKRILOASGIDETVYPRSSSENITMKGRREASTVIRGA 202
Db 114 MEHSLILKDKPSEVPMRILERSGIDETVYPRALHCPAIIPTPTMDAARSAQVIRGA 173
OY 203 LDELFEKTRKPKDGVLYVNCISFNTPPSLSAMVINHYMRGNLSYNLGSGSAGI 262
Db 174 MDLFEKTKGLPKDVIDILVNCISLSPSPSLAMVINHYMRGNLSYNLGSGSAGI 233
OY 263 AILDARDMLQSNPSYAVVSTWVGWVGSDDKSVIPNCFFPMGSAVLSNRRDF 322
Db 234 SVDLARDLQVHPNSNALTIVSTETIPYVGENEAMTLIPNCLFPMGSAVLSNRRDF 293
OY 323 RHAKRYLEHIVTHKAADRSFRSVYQEEDEOGFKLISRDIMEVGEALKTNTTLP 382
Db 294 WRAKRYLEHIVTHKAADRSFRSVYQEEDEOGFKLISRDIMEVGEALKTNTTLP 353
OY 383 LVLPSSEQLFPALALRRTSPAAKTSTTTSFSTATAKINGIKSSSDLSKRYIPDYK 441
Db 354 LVLPSSEQLFPALALRRTSPAAKTSTTTSFSTATAKINGIKSSSDLSKRYIPDYK 386
OY 442 LAFFHCFHAGRAVIDELEKNLGLSEENMEASRMTLHRFGNTSSGIWEELAYMEAKES 501
Db 387 LAFFHCFHAGRAVIDELEKNLGLSEENMEASRMTLHRFGNTSSGIWEELAYMEAKES 446
OY 502 VRRGRVMOIARSGFKNSVYKARKYKPTNNPWDCINRYVPL 548
Db 447 VRRGRVMOIARSGFKNSVYKARKYKPTNNPWDCINRYVPL 492

RESULT 6
US-09-892-325-4

; Sequence 4, Application US/09892325
; Patent No. US20020116735A1
; GENERAL INFORMATION:
; APPLICANT: Kunst et al.
; TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
; Involved in Very Long Chain Fatty Acid Synthesis
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

```

1 ADDRESS: Klarguist Sparkman Campbell
2 Leigh & Whinston, LLP
3 STREET: One World Trade Center, Suite
4 1600, 121 S.W. Salmon Street
5 CITY: Portland
6 STATE: OR
7 COUNTRY: USA
8 ZIP: 97204-2988
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Disk, 3.5-Inch
12 OPERATING SYSTEM: Windows NT
13 SOFTWARE: Word97 & ASCII
14
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: 09/09/892,325
17 FILING DATE: 26-Jun-2001
18 CLASSIFICATION: <Unknown>
19
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 09/058,947
22 FILING DATE: <Unknown>
23
24 ATTORNEY/AGENT INFORMATION:
25 NAME: David J. Earp, Ph.D.
26 REGISTRATION NUMBER: 41,401
27 REFERENCE/DOCKET NUMBER: 5493-50032/DJE
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (503) 226-7391
30 TELEFAX: (503) 228-9446
31
32 INFORMATION FOR SEQ ID NO: 4:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 497
35 TYPE: amino acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38
39 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
40
41 US-09-892-325-4
42
43 Query Match 50.7%; Score 1445; DB 10: Length 497;
44 Best Local Similarity. 53.9%; Pred. No. 8,5e-126;
45 Matches 278; Conservative 93; Mismatches 107; Indels 38; Gaps
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[illegible]

```

; Sequence 42, Application US/09877476
; Patent No. US2002004994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 506
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 399 amino acids from B. napus elongase KCS (SEQ
; OTHER INFORMATION: ID NO:3) and 3' 107 amino acids from A. thaliana
; OTHER INFORMATION: FAE1 (SEQ ID NO:1) having a mutation at residue
; OTHER INFORMATION: 306; designated Bn399 G307D; hypothetical
US-09-877-476-42

```

```

Query Match          42.1%; Score 1200; DB 10; Length 506;
Best Local Similarity 45.2%; Pred. No. 5.3e-103;
Matches 235; Conservative 98; Mismatches 143; Indels 42; Gaps 7;

```

```

QY 43 LOSVNLKYYKLGHYILNHAVALTIPVLYLVSFAEYGSLSREIIMKKMDY---DLATV 99
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MTSIN--VKLHYHYITNLFNLCFFPLTAIV-AGRAYLTIDDLHLHYSLQHNLI 56
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 100 IGFGVFLVACVYFMRSPRSVYLIDPACYKPSDEHVTKEEFTEL-----ARKSG 151
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 APPLAFVFGSVLYIATRPVYLYVESCYLPPTHCHSSISKVMDIFQYRKADPSRNGT 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 152 FDEET-IGFKRILQASGIDETVYPRSSISENITTMKGRERASTVIFGALDELFEKT 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 CDDSSWLDLFRKIQERSGLDDETHGPEGLQVPRKTFARARETEQYIIGALENLFKNT 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 211 RVKPKDGVLYVNCISFNPPSLSAMVINHYKMGKNTLSYLGMGCSAGIATDLARDM 270
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 NVNPKDGLLVNNSMNPPLSLAMVYNTFKLSNVRSNLSGMSAGIATDLAKDL 236
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 271 LOSNPNSYAVVSTEWGIMWYVSDKSMVTPNCFPMGCSAVMLSNRRDFFRAKYLE 330
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 237 LHVHKNYALVSTENTYNTIYAGDNRSAMVSNCLFVVGAAIILSNKPPDRRSKYLEV 296
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 331 HVIATKAAADRFRSRYQEDGEGFKGISRDLMVEGGEALKTNTITGPIVLPSEQ 390
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 297 HVIATKGAADKSRFCVQGDDENGKIGVSLKDTIDVAGRYTKKNTATGPIVLPSEK 356
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 391 LLEFPAALLRFTFSPAATSTTTSFSTATKNTGKSSSSDLSPYIPDKLAFEHFCFH 450
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 357 LLEFVTFM-----GKLFKDKIKHYVDPFKLAIDHFCIH 391
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 451 AASKVYLELOKNGLSENNMEASRMTLHFRGNTSSSGIWEYELAYMAKESVRGRDVMQ 510
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 392 AGGRAVIDLEKNGLSPIDVEASRSTLHFRGNTSSSIWEYELAYIEPKMKKGNKRWQ 451
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 511 IAFSGFKCSNVYKAMRKVKKPTRRNPWDCINRYVPL 550
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 452 IALGSGFKCSAVWALNVKAS- KASANSFWCHCIDRYPKI 490
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RESULT 9
US-09-877-476-6
; Sequence 6, Application US/09877476
; Patent No. US2002004994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.

```

```

; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 505
; TYPE: PRP
; ORGANISM: Brassica napus
US-09-877-476-6

```

```

Query Match          42.0%; Score 1197.5; DB 10; Length 505;
Best Local Similarity 45.2%; Pred. No. 9e-103;
Matches 235; Conservative 96; Mismatches 146; Indels 43; Gaps 7;

```

```

QY 43 LOSVNLKYYKLGHYILNHAVALTIPVLYLVSFAEYGSLSREIIMKKMDY---DLATV 99
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MTSIN--VKLHYHYITNLFNLCFFPLTAIV-AGRAYLTIDDLHLHYSLQHNLI 55
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 100 IGFGVFLVACVYFMRSPRSVYLIDPACYKPSDEHVTKEEFTEL-----ARKSG 151
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 56 APPLAFVFGSVLYIATRPVYLYVESCYLPPTHCHSSISKVMDIFQYRKADPSRNGT 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 152 FDEET-IGFKRILQASGIDETVYPRSSISENITTMKGRERASTVIFGALDELFEKT 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 116 CDDSSWLDLFRKIQERSGLDDETHGPEGLQVPRKTFARARETEQYIIGALENLFKNT 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 211 RVKPKDGVLYVNCISFNPPSLSAMVINHYKMGKNTLSYLGMGCSAGIATDLARDM 270
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 176 NVNPKDGLLVNNSMNPPLSLAMVYNTFKLSNVRSNLSGMSAGIATDLAKDL 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 271 LOSNPNSYAVVSTEWGIMWYVSDKSMVTPNCFPMGCSAVMLSNRRDFFRAKYLE 330
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Db 236 LHVHKNYALVSTENTYNTIYAGDNRSAMVSNCLFVVGAAIILSNKPPDRRSKYLEV 295
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QY 331 HVIATKAAADRFRSRYQEDGEGFKGISRDLMVEGGEALKTNTITGPIVLPSEQ 390
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 296 HVIATKGAADKSRFCVQGDDENGKIGVSLKDTIDVAGRYTKKNTATGPIVLPSEK 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 391 LLEFPAALLRFTFSPAATSTTTSFSTATKNTGKSSSSDLSPYIPDKLAFEHFCFH 450
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 356 LLEFVTFM-----GKLFKDKIKHYVDPFKLAIDHFCIH 390
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 451 AASKVYLELOKNGLSENNMEASRMTLHFRGNTSSSGIWEYELAYMAKESVRGRDVMQ 510
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 391 AGGRAVIDLEKNGLSPIDVEASRSTLHFRGNTSSSIWEYELAYIEPKMKKGNKRWQ 450
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 511 IAFSGFKCSNVYKAMRKVKKPTRRNPWDCINRYVPL 550
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 451 IALGSGFKCSAVWALNVKAS- NSPWECHCIDRYPKI 489
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RESULT 10
US-09-883-797-4
; Sequence 4, Application US/09883797
; Patent No. US2002006123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4

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Db 177 NVNKRDIILVNSMFMPTSLAMVYNTFKLSNVRSFNLGCGCAGVIAIDLADL 236
QY 271 LOSPNISAAVYVSTEMYQYNYVSDKSMVLPNCFEFRGCAVMSNRDRFRRAKYLE 330
Db 237 LHVKNYALVYVSTEMYNTYNTYACDNRSMVSNCLFVRGGAIIILSNPGRDRRSKYLEV 296
QY 331 HYVTHAADDRSRYSYQOEDEOGFKLISRDIMEVGEALNTTTTGLVLPSPSQ 390
Db 297 HYVTHGADDKSRFCYQGGDENGKIGVLSKIDITVAGHTYAKNTATLGLPLSEK 356
QY 391 LLEFPAALLRTFSPAATSTTTSTSTATKNGIKSSSDLSKPYIPDYKLAPEHCFH 450
Db 357 LLEFVTFM-----GKLFKDKIKHYVYDPFKLADHCFH 391
QY 451 AASKVYLELOKNLGLSEENMEASRMTLHREGNTSSGITYELAYEAKESVRRGDWRWQ 510
Db 392 AGGRAVIDLEKNTALAPIDVEASRSTLHREGNTSSSIWELAYIEAKGMRKGNK 451
QY 511 IAFSGFKCNSVVKAMRKVKKPTRNPNWDCINRYVPVL 550
Db 452 IALGSGFKCNSAVWVALRNKAST-NSPWEHCIDRIYVKI 490

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RESULT 15

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US-09-877-476-2
; Sequence 2, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-877-476-2

```

Query Match 41.6%; Score 1186; DB 10; Length 506;
Best Local Similarity 45.5%; Pred. No. 1,1e-101;

Matches 238; Conservative 87; Mismatches 150; Indels 48; Gaps 6;

```

QY 43 LOSVNLKYVKGHYHILINHAVALTIPVLVLFSAEYGSLSREI-----WKKLMDYDLA 97
Db 1 MTSVN--VLLRYVYLTNFENCLPPLTFL---AGKASRLTINDLHNFSLYLQHNLI 53
QY 98 TVIGFGVFLVACVYFMSRPSVYLIDFACYPSDEHKVTKKEFTL-----AR 147
Db 54 TVTLTALFTYVGLVLYTRPNPVYLVDSYCLPPHLKVSYSKVMDFYQIKKADTSR 113
QY 148 KSGKFEDETLGFKRILOASIGDETYVPRSSISENITMKGREASTVIFGALDEL 207
Db 114 NVACDDPSLDLFLKTOERSGLADETSPBGLIHVPKRFTFAASRETEREVIIGALENLF 173
QY 208 EKTRVKKVGVLYVNCISIFNPPLSLAMVINHYKRGNTLSYNLGMCAGIIDA 267
Db 174 EMTKYVPREIGILVNSMFPPLSLAMVNTFKLSNKSINFLGMCAGIIDA 233
QY 268 RDLQSNPNSYAVVSTEMVGNMYGSDKSAVTPNCFPRMCSAVMLSNRRDRPHAKY 327
Db 234 KDLHVHKNYALVYVSTEMITQIYAGEBRSKMSVSNCLFRVGGAIIILSNKSGDRRSKY 293
QY 328 RLEHIVRTHKADDSFRSYQOEDEOGFKLISRDIMEVGEALKTNTTGLVLP 387
Db 294 KLVHIVRTHGADDSFRFCYQGGDENGKIGVLSKIDITVAGTTLTKNIATLGLPL 353

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QY 388 SEQLLEFPAALLRTFSPAATSTTTSTSTATKNGIKSSSDLSKPYIPDYKLAPEH 447
Db 354 SEKLFRTFYAK-----KLLKDKIKHYVYDPFKLADVDF 388
QY 448 CFHASKVYLELOKNLGLSEENMEASRMTLHREGNTSSGITYELAYEAKESVRRGDR 507
Db 389 CIHAGRAVIDLEKNTALAPIDVEASRSTLHREGNTSSSIWELAYIEAKGMRKGNK 448
QY 508 VMOIAFSGFKCNSVVKAMRKVKKPTRNPNWDCINRYVPVL 550
Db 449 AMOIALGSGFKCNSAVWVALRNKAST-KASANSPOHCIDRIYVKI 490

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Search completed: May 11, 2003, 01:33:12
Job time : 614 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2003, 22:59:09 ; Search time 589 Seconds

(Without alignments)
89.769 Million cell updates/sec

Title: US-09-905-657-2

Perfect score: 2848
Sequence: 1 MGRSNEODLLSTEIVNRGIE.....KKPTRRNPWVCINRYPVPL 550

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2848	100.0	550	2	B84658	beta-ketoacyl-CoA
2	1569	55.1	516	2	B86327	protein F18014.21
3	1494.5	52.5	509	2	A84653	probable beta-keto
4	1492	52.4	512	2	F84538	probable beta-keto
5	1459	51.2	528	2	T00951	probable 3-oxoacyl
6	1445	50.7	497	2	T52308	very-long-chain fa
7	1441	50.6	528	2	F86141	protein T25K16.11
8	1402	49.2	487	2	T05271	probable 3-oxoacyl
9	1372	48.2	492	2	F86384	probable protein f
10	1213	42.6	451	2	T49095	beta-ketoacyl-CoA
11	1197.5	42.0	505	2	T07900	probable 3-oxoacyl
12	1196.5	42.0	466	2	D84906	probable beta-keto
13	1194	41.9	493	2	T04771	fatty acid elongas
14	1186	41.6	506	2	T05272	fatty acid elongas
15	1180	41.4	506	2	T07934	probable 3-oxoacyl
16	1170.5	41.1	476	2	H84524	probable fatty aci
17	1005.5	35.3	460	2	C96736	probable ketoacyl-
18	844	29.6	478	2	D86212	hypothetical prote
19	822	28.9	464	2	T48449	fatty acid elongas
20	817.5	28.7	476	2	C84687	probable fatty aci
21	495.5	17.4	168	2	T07846	probable beta-keto
22	486.5	17.1	168	2	T07845	beta-ketoacyl synt
23	482.5	16.9	168	2	T14434	probable beta-keto
24	481.5	16.9	168	2	T14385	fatty acid elongas
25	213	7.5	438	2	C75587	probable chalcone
26	181.5	6.4	365	2	A69593	naringenin-chalcon
27	179	6.3	325	2	B97339	naringenin-chalcon
28	175	6.1	353	2	G70621	probable chalcones
29	167	5.9	388	2	S60472	naringenin-chalcon

30	166.5	5.8	388	1	SYSCN	naringenin-chalcon
31	166.5	5.8	388	2	JQ2259	naringenin-chalcon
32	166	5.8	391	2	T10713	naringenin-chalcon
33	163.5	5.7	388	1	SYSC1	naringenin-chalcon
34	163	5.7	388	2	JQ2249	naringenin-chalcon
35	160.5	5.6	324	2	D81452	3-oxoacyl-lacyl-ca
36	156	5.5	388	1	SYSC3	naringenin-chalcon
37	156	5.5	390	2	T10231	another-specific pr
38	156	5.5	398	2	S42523	naringenin-chalcon
39	156	5.5	402	2	S5465	chalcone synthase
40	154.5	5.4	389	1	SYFUCP	naringenin-chalcon
41	154	5.4	363	2	T15054	another-specific pr
42	154	5.4	419	1	SYPCD	naringenin-chalcon
43	153	5.4	388	2	S37098	naringenin-chalcon
44	153	5.4	389	2	S35163	naringenin-chalcon
45	153	5.4	392	2	S53313	stilbene synthase

ALIGNMENTS

RESULT 1	
B84658	beta-ketoacyl-CoA synthase (FIDDLEHEAD) [imported] - Arabidopsis thaliana
C:Species:	Arabidopsis thaliana (mouse-ear cress)
C:Date:	02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession:	B84658
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKien, S.E.; Umayan, L.; Tallon euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999	
After sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.	
A:Reference number:	A84420; MUID:20083487; PMID:10617197
A:Accession:	B84658
A:Status:	Preliminary
A:Molecule type:	DNA
A:Residues:	1-550 <STO>
A:Cross-references:	GB:A8002093; NID:g3075394; PIDN:AC14526.1; GSPDB:GN00139
C:Genetics:	
A:Gene:	At2g26250
A:Map position:	2
Query Match	
Best Local Similarity	100.0%; Score 2848; DB 2; Length 550;
100.0%; Pred. No. 1.5e-205;	
Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 MGRSNEODLLSTEIVNRGIEPSGNAGSPFESVRRRLPDFLQSVNLRKYVGLGYHLIN 60
DB	1 MGRSNEODLLSTEIVNRGIEPSGNAGSPFESVRRRLPDFLQSVNLRKYVGLGYHLIN 60
OY	61 HAVYATTPVLVLSAEVGSLSREIWKLLMDYLAIVIGFGVFLTACYEFMSRRS 120
DB	61 HAVYATTPVLVLSAEVGSLSREIWKLLMDYLAIVIGFGVFLTACYEFMSRRS 120
OY	121 VYLIDFACYPKSDHKVTKKEFIELARKSGKDEETLFGKKIILQASGIGDETYPRIS 180
DB	121 VYLIDFACYPKSDHKVTKKEFIELARKSGKDEETLFGKKIILQASGIGDETYPRIS 180
OY	181 SSENITMKEGREASVYIFGALDELFEKTRVAPKDVGVLVVNCISFNPBPSLSAMVIN 240
DB	181 SSENITMKEGREASVYIFGALDELFEKTRVAPKDVGVLVVNCISFNPBPSLSAMVIN 240
OY	241 YKMRNIIISYNGMGCSAGIATLADMDQSNNSVAVVSTMGVNMVVGSDKSNV 300
DB	241 YKMRNIIISYNGMGCSAGIATLADMDQSNNSVAVVSTMGVNMVVGSDKSNV 300
OY	301 IPNCFRFGCSAVMLSNRRDFRHAQYRLHIVRTHKAADRSFVSVOEEDQGFGLK 360
DB	301 IPNCFRFGCSAVMLSNRRDFRHAQYRLHIVRTHKAADRSFVSVOEEDQGFGLK 360
OY	361 ISRDIMEVGEALKTNTTGLPLVPFSBQLFPFALLRRFSPPAKSTTTSSTATA 420
DB	361 ISRDIMEVGEALKTNTTGLPLVPFSBQLFPFALLRRFSPPAKSTTTSSTATA 420

QY 421 KTINGISSSDLSKPYIPDYKLAFEHCFHASKVYLELOKNGLSEENMEASRMTLHR 480
 DB 421 KTINGISSSDLSKPYIPDYKLAFEHCFHASKVYLELOKNGLSEENMEASRMTLHR 480
 QY 481 FGTSSSGIWEYELAYWEAKESVRGRDQVQIAFGSGFKCNVYKAMRKVKRPTNNPVY 540
 DB 481 FGTSSSGIWEYELAYWEAKESVRGRDQVQIAFGSGFKCNVYKAMRKVKRPTNNPVY 540
 QY 541 DCINRYPVPL 550
 DB 541 DCINRYPVPL 550

RESULT 2

Protein F18014.21 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 R:Phenology: A.; Ecker, J.R.; Palm, C.J.; Federle, N.A.; Kaul, S.; White, O.; Alonso,
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Nansen, N.F.; Hughes, B.; Hutzlar, L.
 A:Accession: F66327
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, X.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Ventier, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: F66327
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-516 <STO>
 A:Cross-references: GB:AE005172; NID:98778420; PID:AAF9428.1; GSPDB:GN00141
 A:Genetics:
 A:Gene: F18014.21
 A:Map position: 1

Query Match 55.1%; Score 1569; DB 2; Length 516;
 Best Local Similarity 56.5%; Pred. No. 1,1e-109;
 Matches 300; Conservative 82; Mismatches 117; Indels 32; Gaps 5;

QY 23 GPNAGSTFSTFVRARRLPDLQSNVNLKYKGYHLINHAVALTIPIVLFSAEVSGL 82
 DB 13 GGGGSGVGVQIRQTRMLPDLQSNVNLKYKGYHLINHAVALTIPIVLFSAEVSGL 82
 QY 83 SREIRWKLW---DYDLATVIGFGVFLVACVYFMSRPSVYLIDPACVPSDEHKVTK 139
 DB 72 NPDDL KQIMIHQYINLVSTIISGAILVFGILVYVMTRPVYLVDFSCYLPDHLKAPY 130
 QY 140 EEFTELARKSGKDETELGFKKRILOASGIDETVYPRSSISENITTMKREGREASTVI 199
 DB 131 ARMEHSLRLGDDDSALFQRKILERSGIDETVYPRSSISENITTMKREGREASTVI 199
 QY 200 FGLDELFEFTRKPKDVGVLVNCSTFNPPLSAMVINHYKMGNTLSYNLGMCSSA 259
 DB 191 FGLDMLFANTVYKPKDIGILVNCSTFNPPLSAMVINHYKMGNTLSYNLGMCSSA 250
 QY 260 GIAIDLARDMLQSNVYAVVSTEWGINKVVGSKSVITNCFPRMCCSAVMLSNRR 319
 DB 251 GYAVAVLADMLLVHRTAVVSTENITQWYFGNKKSMILINCLFRVGSAYVLSNKS 310
 QY 320 RDRHAKYRLVHTVTHKAADRSFRSVYOEDEOGFKGLISRDLMVGEALKTNTTT 379
 DB 311 RDRHAKYRLVHTVTHKAADRSFRSVYOEDEOGFKGLISRDLMVGEALKTNTTT 370
 QY 380 LGPLVLPSEQLLFFAALLRRTFSPAKTSTTSTSTATAKNGIKSSSDLSKPYID 439
 DB 371 LGPLVLPSEQLLFFAALLRRTFSPAKTSTTSTSTATAKNGIKSSSDLSKPYID 404
 QY 440 YKLAPHFCHFAASKVYLELOKNGLSEENMEASRMTLHFGNTSSSGIWEYELAYWEAK 499

DB 405 FKLAFEHCFCHAGRAVIADELEKNQLSPVYDASRMTLHFGNTSSSGIWEYELAYWEAK 464
 QY 500 ESVRGRDQVQIAFGSGFKCNVYKAMRKVKRPTNNPVQICINRYPVPL 550
 DB 465 GRMRGRDQVQIAFGSGFKCNVYKAMRKVKRPTNNPVQICINRYPVPL 514

RESULT 3

Probable beta-ketoacyl-CoA synthase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: A84663
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Unayam, L.; Tallon,
 eus, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ven-
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: A84663
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-509 <STO>
 A:Cross-references: GB:AE002093; NID:92760830; PID:AA95298.1; GSPDB:GN00139
 A:Genetics:
 A:Gene: AC2426640
 A:Map position: 2

Query Match 52.5%; Score 1494.5; DB 2; Length 509;
 Best Local Similarity 54.8%; Pred. No. 4e-104;
 Matches 283; Conservative 88; Mismatches 112; Indels 33; Gaps 5;

QY 37 RRLPDLQSNVNLKYKGYHLINHAVALTIPIVLFSAEVSGLSREIRWKLW--- 93
 DB 15 RRLPDLQSNVNLKYKGYHLINHAVALTIPIVLFSAEVSGLSREIRWKLW--- 93
 QY 94 YDLATVIGFGVFLVACVYFMSRPSVYLIDPACVPSDEHKVTKKEFTELARKSGKFD 153
 DB 73 YNLISVAVGSMVLVFLMTIYFMTRPVYLVNFCFPRDESRCKTKIFMDRSKLTGSEFT 132
 QY 154 EETLGFKKRILOASGIDETVYPRSSISENITTMKREGREASTVIIGALDELFEKTRVK 213
 DB 133 EENLEFQKRILOASGIDETVYPRSSISENITTMKREGREASTVIIGALDELFEKTRVK 213
 QY 214 PKDVGVLVNCSTFNPPLSAMVINHYKMGNTLSYNLGMCSSAGIATDLARDMLQS 273
 DB 193 PKDIGILVNCSTFNPPLSAMVINHYKMGNTLSYNLGMCSSAGIATDLARDMLQS 252
 QY 274 NPNSYAVVSTEWGINKVVGSKSVITNCFPRMCCSAVMLSNRRDPRHAKYRLVHT 333
 DB 253 IPNTYAVVSTEWGINKVVGSKSVITNCFPRMCCSAVMLSNRRDPRHAKYRLVHT 312
 QY 334 RTHKAADRSFRSVYOEDEOGFKGLISRDLMVGEALKTNTTTGRLVLPSEQLL 393
 DB 313 RTHKAADRSFRSVYOEDEOGFKGLISRDLMVGEALKTNTTTGRLVLPSEQLL 372
 QY 394 FALLL-RTFSPAKTSTTSTSTATAKNGIKSSSDLSKPYIDPYKLAFEHCFHAA 452
 DB 373 FALVLRKLEFKMKI-----KRIYDFKLAFEHCFCHAG 405
 QY 453 SKYVLELOKNGLSEENMEASRMTLHFGNTSSSGIWEYELAYWEAKESVRGRDQVQIA 512
 DB 406 GRAVIADELEKNQLSPVYDASRMTLHFGNTSSSGIWEYELAYWEAKESVRGRDQVQIA 465
 QY 513 FGSFGKCNVYKAMRKVKRPTNNPVQICINRYPV 548
 DB 466 FGSFGKCNVYKAMRKVKRPTNNPVQICINRYPV 501

RESULT 4

F84538
 Probable beta-ketoacyl-CoA synthase [imported] - Arabidopsis thaliana

C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: F84538
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffitt, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.;
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84538
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-512 <STO>
A:Cross-references: GB:AE002093; NID:g4544399; PIDN:AMD22309.1; GSPDB:GN00139
C:Genetics:
A:Map: AT2g16280
A:Map position: 2

Query Match	52.48;	Score 1492;	DB 2;	Length 512;
Best Local Similarity	54.18;	Pred. No. 6.2e-104;		
Matches, 280;	Conservative 100;	Mismatches 106;	Indels 32;	Gaps 6;

[illegible]

RESULT 5
 T00951
 Probable 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) F20D22.1 - Arabidopsis
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Jul-1999
 C:Accession: T00951
 R:Vytotskai, V.S.; Osborne, B.I.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji, C.
 K.; Feng, J.; Kim, C.; Kurtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.;
 submitted to the EMBL Data Library, May 1998
 A:Description: Arabidopsis thaliana chromosome 1 BAC F20D22 complete sequence.
 A:Reference number: Z14214
 A:Accession: T00951
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-528 <VYS>
A:Cross-references: EMBL:NC002411; NID:g2570223; PTD:g3142289
C:Genetics:
A:Map position: 1
A:Introns: 256/3
A:Note: F20D22.1
C:Keywords: acyltransferase

query Match	51.2%;	Score 1459;	DB 2;	Length 528;
Best Local Similarity	53.4%;	Pred. No. 1.9e-101;		
Matches 278;	Conservative 91;	Mismatches 120;	Indels 32;	Gaps 5;

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0Y 37 RLRLPELOSVNKLYKGLGYHYLIINHAVALATPVLVLYESAQVSLIS--REETIKMLMD 95
Db 20 KILPFLISVRKLYKGLGYHYLIINHAVALIILPVLGLAATSSPSFTDLTLXNHLAKFH 79
0Y 96 IATVIGPGEVLTACVYFMSRPSVLYLIDFACVYPSDEHKVYKEEFTELAKSGKPDDE 155
Db 80 FLSTSLFALLTLFTLTLVFTTRPRRIFLIDFACVYPPDSLSLICTRETFPMDSORVGIETFD 139
0Y 156 TLGFEKKRILQASGIDENYVPRSSISENITTMKGRREASVINGALDELPEKTRVYPK 215
Db 140 NLAPQOKILERSGLQOKITFPALLRVPPNPPCMSEKRAEATVMTGADVALEKTVANK 199
0Y 216 DVGVYVNVCSINPPPSISAMVINHYKMRGNLTLYNLGMSGCSAGIILADLARDMOSNP 275
Db 200 DIGILVNVCSLEPNPPSISAMIVNKYKILRGVLTLYNLGMSGCSAGIISIDLAKQLQVOP 259
0Y 276 NSYAYVYSTEAMGYWMYVGSDBKSAYITPNCFFPMGCSAVALSNRRDPFRAKRLLEHYRT 335
Db 260 NSYALVYSTEMLTWLYLGNDRSMLLNSCIFPMGGAVALSNRRSDRCSKQYLJHYVAT 319
0Y 336 HRAADDRSPRSYVQOEDEQFGR--GLKISRDLMEVGEALKNITITLGLVYFPSEOLLE 393
Db 320 HKSQDNMFNCYVQEDNDNDNKQIGVLSKLNMAIAGELKNTNITTIGLVLVPMEOELLE 379
0Y 394 FPAALRRFTSPAKTSTTTSBSTSATAKTNGIKSSSSDLISKPYIDPYKLAFFHCFPHAA 453
Db 380 FPAIVAR-----KVFNVK-----IKPYIDPFKLAFFHCFIHAAG 414
0Y 454 KYVLEELQNLKLTSEENMEASRMTLHRFGNTSSSGIMVLEYLAWEAKESVRRODRYQWAL 513
Db 415 RAYVDEIEKENLDLSEHMEHPSRMTLNRFGNTSSSSIMVLEYLAWEAKESGRKIKRDRYQWAL 474
0Y 514 GSGFCNSVYWKAMKV---KKPLRNPWDVCINRIYVPL 550
Db 475 GSGFCNSAVMRALKTIDPSEKRRKKNTPWIDEIHEFPV 515

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RESULT 6
T52308
very-long-chain fatty acid condensing enzyme CUT1 [validated] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C:Accession: T52308
R:Miller, A.A.; Clemens, S.; Zaehgo, S.; Ghiblin, M.; Taylor, D.C.; Kunst, L.
Plant Cell 11, 825-538, 1999
A:Title: CUT1, an Arabidopsis gene required for cuticular wax biosynthesis and pollen
A:Reference number: Z52032; MUID:99264304; PMID:10330468
A:Accession: T52308
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-497 <MIL>
A:Cross-references: EMBL:AF129511; PIDD:ADD37122.1
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: CUT1
C:Function:
A:Description: necessary for cuticular wax production [validated, MUID:99264304]; pro
Query Match          50.7%; Score 1445; DB 2; Length 497;
Best Local Similarity 53.9%; Pred. No. 2e-100;
Matches 278; Conservative 93; Mismatches 107; Indels 38; Gaps 8;

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protein T25K16.11 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F86141
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Hughes, B.B.; Conn, D.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,
Nature 408, 815-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maltli, R.; Marzalli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F86141
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-528 <STO>
A:Cross-references: GB:AE005172; NID:96715643; PIDN:AE26470.1; GSPDB:GN00141
C:Genetics:
A:Gene: T25K16.11
A:Map position: 1

Query Match	50.6%	Score 1441	DB 2	Length 528
Best Local Similarity	51.2%	Pred. No. 4,3e-100		
Matches 288	Conservative 97	MSMatches 124	Indels 54	Gaps 11
QY	1	MGRSN----	EODLSEINRGICPEPAGAGPTSVKRRLLPDFLOSVNLTQYKLGTH	56
			:::	
Db	1	MERTSIEMDRRLVLAEMAFR-----	-DSSASVIRIRRLPDLTSLSVKRLKYKLGTH	51
OY	57	YLINHA--YLATIP-----	VLVYFSAEAGVSLSREELW-KLIMWYDLYATIG--FFGVF	106

RESULT 8
 T05271
 Probable 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) - *Arabidopsis thaliana*
 N/Alternate names: ketoacyl-CoA synthase; protein T4L20.90
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
 C/Accession: T05271
 R:Bevan, M.; Terrin, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.;
 Ewens, H.W.; Mayer, K.F.X.; Schueller, C.
 Submitted to the Protein Sequence Database, September 1998
 A:Reference number: Z15406
 A:Accession: T05271
 A:Molecule type: DNA
 A:Residues: 1487 <BEV>
 A:Cross-References: EMBL:AL023094
 A:Experimental source: cultivar Columbia; BAC clone T4L20
 C:Genetics:
 A:Map position: 4
 A:Note: T4L20.90
 C:Keywords: acyltransferase

Query Match	49.28;	Score 1402;	DB 2;	Length 487;
Best Local Similarity	53.7%;	Pred. No. 3.2e-97;		
Matches	273;	Conservative	89;	Mismatches 102; Indels 44; Gaps 8;
OY	50	YKLCGHVYLINNAVYIATIPVLVLF-SAEVGSLSREELMKIMLDYLATVIGFGVFYL	108	
		: : : : : : : : :		
Dd	15	YKLGTHVLIITFFKILMFPLMAVALEMNYSLSLNLHLYL-----YNST---GF--IPVI	64	
OY	109	T-----ACVYFMSRRSVYLLIDPACYKDSDEHKVTKEEFIELARKSGKFEDETLGKKRI	163	
		: : : : : : : : :		
Dd	65	TLAIVGSIVTFEFSRBSRSIYLLDSCYLPSSQKVSYQAFMNNSSLIQPFSETSLEFKRKI	124	
		: : : : : : : : : :		
OY	164	LQASIGDETVPKRISSENENITTKKEEREAASVIFGALDELFEKTRVKPKDVGLVNVN	223	
		: : : : :		
Dd	125	LIRSLGGETYLLPDPSIHSHIPRPPTMAAREAEQYIFGALDNLTENTKINIRETGVLVVN	184	
		: : : : :		

Db 351 -----EPGFHICVLASSKRYLDDIHKDKLLEENMEASRTLERGNTSSSI 399

QY 490 WYELAYEAKSVRGDRWQIAFGSKNSVYWKARKYKPTRRNPW 539

Db 400 WYELAYEAKSVRGDRWQIAFGSKNSVYWKARKYKPTRRNPW 449

RESULT 11

T07900

Probable 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) FAE1 - rape

N:Alternate names: 3-ketoacyl-CoA synthetase; fatty acid elongase

C:Species: Brassica napus (rape)

C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999

C:Accession: T07900

R:Roscoe, T.J.; Domergue, F.; Lessire, R.; Delseeny, M.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z16199

A:Accession: T07900

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1505 <ROS>

A:Cross-references: EMBL:U05071; NID:q1255206; PIDN:AAA96054.1; PID:q1255207

C:Genetics:

A:Gene: FAE1

C:Function:

A:Description: catalyzes the transfer of malonyl from malonyl-CoA to the fatty acid chain

A:Pathway: fatty acid synthesis

C:Keywords: acyltransferase

Query Match 42.0%; Score 1197.5; DB 2; Length 505;

Best Local Similarity 45.2%; Pred. No. 7.3e-82;

Matches 225; Conservative 96; Mismatches 146; Indels 43; Gaps 7;

QY 43 LQSYNLKYLKHYLLINHAVALTIPVLVFSAEVGSLSREIWKLMYD---DLATV 99

Db 1 MTSIN--VKLLHYVTINLFNLCFFPLTAIV--AGKAYLTIDDLHLHYSLQHNLTIT 55

QY 100 IGFGEVFLVACVYFMRPSVYLIDPACYKPSDEHKYTKKEFEL-----ARKSGK 151

Db 56 APLLAFTVGSVLIATRPVYLVESCYLPTHCSSISKVNDIFFOYKADPSRNGT 115

QY 152 FDEET-LGFKRRLQASIGIDETVYPRSSISENITMKREGEASVIFGALDELFEKT 210

Db 116 CDDSMWDLFRKIQERSGLDETHGPBGLOVPPRKTFARARETEQVYIIGALENLKNT 175

QY 211 RVPKDVGLVYVNCSTNPPLSLAMVINYKMGKNTLSYNGMGCSAGIATDARDM 270

Db 176 NVNPKVDIGLVVNSMNPPLSLAMVINYKMGKNTLSYNGMGCSAGIATDARDM 235

QY 271 LQSNPNYAVVSTEMVYGVMMYGSQSMVLPNCFRFGCSAVWLSNRDRDFRAKTRLE 330

Db 236 LHVHKTALVAVSTENTITVYIAGDNKSMVSNCLFVVGAAIILSKPPDRRSKYLEV 295

QY 331 HAVTHAADRSFVYQDEDEGFKGLKISRLMEVGEALKTNTTIGPLVLPSEQ 390

Db 296 HAVTHGADKSPRCVQDDEGCGVSLNDITDVAKRYKKNATIGPLILPSEK 355

QY 391 LLEFPAALLRRTFSPAAKSTTTSTSTSAKTGKISSSDLSKPYIDPKLAHEHCFH 450

Db 356 LLEFVTFM-----GKLFKDEIKHYVPPDEKLAIIDHFCIH 390

QY 451 AASKVYLEELQKNGISEENMEASRMTLHFGNTSSGIYELAYMAKESVRGDRWQ 510

Db 391 AGKAVYIDVLEKNGIAPDIVEASRSLHFRGNTSSSIYELAYIPKRMKGNKRWQ 450

QY 511 IAFSGFKNSVYWKARKYKPTRRNPWDCINRYPVPL 550

Db 451 IALGSGFKNSAVVVALNNVAKST-NSPWHCIDIIRYVKI 489

RESULT 12

D84906

Probable beta-ketoacyl-CoA synthase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: D84906

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Koo, H.; Moffat, K.S.; Crobin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: D84906

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1466 <STO>

A:Cross-references: GB:AE002093; NID:q3831446; PIDN:AA69929.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g46720

A:Map position: 2

Query Match 42.0%; Score 1196.5; DB 2; Length 466;

Best Local Similarity 45.8%; Pred. No. 7.7e-82;

Matches 228; Conservative 105; Mismatches 116; Indels 49; Gaps 7;

QY 63 VYLAFTPLVYFSAEVSLSREIWKLMYDILATV-IGFGEV-----VLTACVFE-- 114

Db 3 IAMDFFKILUL-----LISLFEULDHLHHDFFSPVYKIGLLISIFVYA 51

QY 115 -MSRPSVYLIDPACYKPSDEHKYTKKEFELARKSGKPEDETLGFKRRLQASIGIDE 172

Db 52 YSTRSKPVYLVDSCHQPTDSCKISSETFENMAKGNOLYDEITQFMTRLNNSGIGDD 111

QY 173 TYVRSISSSENITMKREGEASVIFGALDELFEKTRVAKDVGLVYVNCSTNPPLS 232

Db 112 TYSRCHMLTSPPTSMYEAHRESELVIFGALNSLFKKTGTGIEPRRGVIFIVNCSLFNPNPS 171

QY 233 LSAMVINYKMGKNTLSYNGMGCSAGIATDARDMLQSNPNYAVVSTEMVYGVMMY 292

Db 172 LSSMIVNRYKTKIDVYKTNLSGMCSSAGALSVDATLNLKANPVTAVYVSTEMTLSMY 231

QY 293 VGSQSMWDLFRKIQERSGLDETHGPBGLOVPPRKTFARARETEQVYIIGALENLKNT 352

Db 232 RGNDRSMVLPNCFRFGCSAVWLSNRDRDFRAKTRLEHVTYRKAADDSFRSYQDEED 291

QY 353 EOGKGLKISRLMEVGEALKTNTTIGPLVLPSEQLFPFALLRRTSSPAKSTTTT 412

Db 292 SKGIVGALSKELTIVAGDSLKTNLTAIGPLVLPSEKLEFIFLVK----- 338

QY 413 SFTSATATKNGIKSSSDLSKPYIDPKLAHEHCFCHAAASKVYLELOKNGISEENME 472

Db 339 -----SKLFRKLV-----PVPDFKLCFKHFCIHAGRALLDVVERGLGISEFDLE 365

QY 473 ASRMTLHFRGNTSSGIYELAYMAKESVRGDRWQIAFGSKNSVYWKARKY-- 530

Db 386 PSRMTLHFRGNTSSSIYELAYEAKCVKRGDRWQIAFGSKNSIYVWALRTIPA 445

QY 531 KKPTRRNPWDCINRYPV 548

Db 446 NESLVNPMGDSVHKYPV 463

RESULT 13

T04771

fatty acid elongase homolog F10M10.20 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999

C:Accession: T04771

R:Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Hohelsel, J.; Mewes, H.W.; May

submitted to the Protein Sequence Database, February 1999

A:Reference number: Z15384

A:Accession: T04771

A:Molecule type: DNA

A:Residues: 1493 <BEV>

A:Cross-references: EMBL:AL035521

A:Experimental source: cultivar Columbia; BAC clone F10M10


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Db 177 NVNPKDIGLVNNSMFPNTPSLSAMVNTFKLRNSVRSFNIGMGCSAGVIAIDLAKDL 236
QY 271 LOSNPNSIAVYVSTEMVGYNNYVGSOKSMVLPNCFRRMGCSAVMLSNRRDRFRAKYRL 330
Db 237 LHVHKNITVAVSTENITYAGDNRSMVSNCLFRVGAAILSNKPGDRRSKYEIV 296
QY 331 HIRTHKAAADRSPFSVYOEDEOGFKLKSRLMEVGEALKTNTITLGPVLPFSEQ 390
Db 297 HTVTHHGADGKSPRCVQGGDENGKIGVSLSKDITVAGRTVKKNITLIGPLILPSEK 356
QY 391 LFFPAALLRRTSPAKTSTTSTSATAKTNGIKSSSDLSKPYIPDYKLAFFHFCFH 450
Db 357 LFFVTFW-----GKLEPKDKIKHYVPDFKLAIDHFCIH 391
QY 451 AASKVYLEELOKNTGLSENNASRMTLHRFGNTSSSGIWEYELAYMEAKESVRGRDRYWO 510
Db 392 AGGRAVIDVEKKNLAPIDVEASRSTLHRFGNTSSSGIWEYELAYIEAKGRKKGNKYWO 451
QY 511 IAFSGFCKNSVWVKARVKKKPTRRNPWVCINRYPVPL 550
Db 452 IALGSGFCKNSAVVVALNNVAKST-NSPWEHCIDRYPVKI 490

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Search completed: May 10, 2003, 23:50:22
 Job time : 592 secs

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2003, 17:59:00 ; Search time 3480 seconds

(without alignments)
12947.082 Million cell updates/sec

Title: US-09-905-657-1

Perfect score: 2782
Sequence: 1 aactaactactctcaccac.....ttacgtgtataagaagatac 2782

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estcov:*
6: em_estcpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	587.4	21.1	589	10	AV781377 AV781377
C 2	574	20.6	574	10	AV565936 AV565936
C 3	573	20.6	573	10	AV522233 AV522233
C 4	544	19.6	544	10	AV529660 AV529660
C 5	526	18.9	526	10	AV560055 AV560055
C 6	504	18.1	504	10	AV566012 AV566012

C 7	494.6	17.8	775	17	BH444293
C 8	493.2	17.7	585	10	AV828119
C 9	493.2	17.7	710	10	AV821120
C 10	474	17.0	474	10	AV560773
C 11	474	17.0	474	10	AV564080
C 12	460.4	16.5	462	10	AV563747
C 13	451.4	16.2	453	10	AV797399
C 14	444.2	16.0	473	10	AV563591
C 15	441.4	15.9	443	10	AV530486
C 16	440	15.8	440	10	AV794790
C 17	432.4	15.5	434	10	AV793345
C 18	431	15.5	431	10	AV796294
C 19	430	15.5	430	10	AV798397
C 20	430	15.5	431	10	AV795796
C 21	426.4	15.3	428	10	AV796196
C 22	426	15.3	542	9	AA651028
C 23	422.2	15.2	427	10	AV808884
C 24	421.2	15.1	565	10	AV559819
C 25	418	15.0	535	10	AV527869
C 26	416	15.0	450	10	AV793380
C 27	412	14.8	412	10	AV562105
C 28	411.8	14.8	415	10	AV786029
C 29	410.4	14.8	413	10	AV815065
C 30	406.8	14.6	422	10	AV810494
C 31	405.4	14.6	408	10	AV815039
C 32	402.4	14.5	404	10	AV806150
C 33	401.2	14.4	591	14	R64812
C 34	401	14.4	402	10	AV814168
C 35	400.4	14.4	445	10	AV440173
C 36	399.8	14.4	426	10	AV799924
C 37	397	14.3	409	10	AV815196
C 38	394.8	14.2	398	10	AV817662
C 39	394	14.2	416	10	AV812808
C 40	389	14.0	409	10	AV817921
C 41	388	13.9	393	10	BE524780
C 42	386.6	13.9	416	10	AV808849
C 43	386	13.9	400	14	T04345
C 44	376.8	13.5	402	10	AV799452
C 45	370.6	13.3	389	10	AV806742

ALIGNMENTS

RESULT 1
LOCUS AV781377/c 589 bp mRNA linear EST 28-MAR-2002
DEFINITION AV781377 RAFL2 Arabidopsis thaliana cDNA clone RAFL02-03-L07 3'
ACCESSION AV781377
VERSION AV781377.1 GI:19800167
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 589)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shingawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rcc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a

modified pBluescript vector as a Setai/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES
Location/Qualifiers

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/db_xref="taxon:3702"
/clone="RAF102-03-107"
/dev_stage="Rosette plants"
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Query Match 21.1%; Score 587.4; DB 10; Length 589;
Best Local Similarity 99.8%; Pred. No. 7.3e-87;
Matches 588; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 589 TTCTCTACCTCCGCCACCGCAAAACCAATGAAATCAAGTCTCTCCATCCGATCTGTC 530
QY 2085 AAGCATATCATCCCGGACTATCAAGCTCCCTTCGACATTTTTCCTCCACGCGCAAGC 2144
DB 529 AAGCATATCATCCCGGACTATCAAGCTCCCTTCGACATTTTTCCTCCACGCGCAAGC 470
QY 2145 AAGTAGTGTGAAGACCTTCAAAAGAAATAGAGCTTGAAGAGAAATATGAGAGCT 2204
DB 469 AAGTAGTGTGAAGACCTTCAAAAGAAATAGAGCTTGAAGAGAAATATGAGAGCT 410
QY 2205 TCTAGATGACATCTCACAGGTTTGGAACACTTCTAGACATGAAATCTGTATGAGTTG 2264
DB 409 TCTAGATGACATCTCACAGGTTTGGAACACTTCTAGACATGAAATCTGTATGAGTTG 350
QY 2265 GCTTACATGAGGCCAAGAAAGTGTGTAGAGCCATAGGTTTGGCAGATCGCTTTC 2324
DB 349 GCTTACATGAGGCCAAGAAAGTGTGTAGAGCCATAGGTTTGGCAGATCGCTTTC 290
QY 2325 GGTCTGTGTTTAAAGTGTACAGTGTGTGTGAAGGCAATGAGAGAGTGAAGAGCCA 2384
DB 289 GGTCTGTGTTTAAAGTGTACAGTGTGTGTGAAGGCAATGAGAGAGTGAAGAGCCA 230
QY 2385 ACCAAGAAACAATCCTTGGGTGATTCATCAACCGTTACCTGTCCTCTTAATATTC 2444
DB 229 ACCAAGAAACAATCCTTGGGTGATTCATCAACCGTTACCTGTCCTCTTAATATTC 170
QY 2445 ATTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2504
DB 169 ATTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 110
QY 2505 TTGATGATGAGAGTATTTACTGATCATCTGATCTAAGTCTGTATTAAGATGATGT 2564
DB 109 TTGATGATGAGAGTATTTACTGATCATCTGATCTAAGTCTGTATTAAGATGATGT 50
QY 2565 GCGTAGAGTCTGTACAGCTTCAACTGTTTATTTTGTGTTGTC 2613
DB 49 GCGTAGAGTCTGTACAGCTTCAACTGTTTATTTTGTGTTGTC 1

RESULT 2
AV565936/c 574 bp mRNA linear EST 07-SEP-2000
LOCUS
DEFINITION
thaliana cDNA clone SQ233403f 3', mRNA sequence.
ACCESSION
AV565936
VERSION
AV565936.1 GI:8737386
KEYWORDS
EST.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 574)
AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Rabata, S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The first laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

FEATURES
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/strain="Columbia"
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Location/Qualifiers

BASE COUNT 176 a 138 c 102 g 158 t
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Query Match 20.6%; Score 574; DB 10; Length 574;
Best Local Similarity 100.0%; Pred. No. 1.2e-84;
Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2073 TCCGATCTGTCCACACCATATCCCGGACTACAGCTCCGCTTGACATTTTGTCTC 2132
DB 574 TCCGATCTGTCCACACCATATCCCGGACTACAGCTCCGCTTGACATTTTGTCTC 515
QY 2133 CACGGGCAAGAAAGTGTGTGAAGCTTCAAAAGAAATCTAGGCTGTGAGAG 2192
DB 514 CACGGGCAAGAAAGTGTGTGAAGCTTCAAAAGAAATCTAGGCTGTGAGAG 455
QY 2193 AATATGAGGCTTCTAGAGTACACATTCACAGGTTTGGAAACATCTTACAGAGTGAATC 2252
DB 454 AATATGAGGCTTCTAGAGTACACATTCACAGGTTTGGAAACATCTTACAGAGTGAATC 395
QY 2253 TGTATGAGTGTGCTTACATGAGGCCAAGAAAGTGTGTGAGAGCGATAGGTTGG 2312
DB 394 TGTATGAGTGTGCTTACATGAGGCCAAGAAAGTGTGTGAGAGCGATAGGTTGG 335
QY 2313 CAGATCGCTTCCGTTTGGTTTAAAGTGTAAAGTGTGTGAGAGCAATGAGAG 2372
DB 334 CAGATCGCTTCCGTTTGGTTTAAAGTGTAAAGTGTGTGAGAGCAATGAGAG 275
QY 2373 GTGAAGAGCCCAACGAGAAACATCCTTGGGTGATTCATCAACCGTTACCTGTGCT 2432
DB 274 GTGAAGAGCCCAACGAGAAACATCCTTGGGTGATTCATCAACCGTTACCTGTGCT 215
QY 2433 CTCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2492
DB 214 CTCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 155
QY 2493 GATACAGTTTGGTGTGATGATAGAGTATTTACTGATCATCTGATTAAGTCTGAT 2552
DB 154 GATACAGTTTGGTGTGATGATAGAGTATTTACTGATCATCTGATTAAGTCTGAT 95
QY 2553 AAGAAATGATGTGCTAGAGTCTGTTCAGCTTCAACTGTTTATTTTGTGTTCT 2612
DB 94 AAGAAATGATGTGCTAGAGTCTGTTCAGCTTCAACTGTTTATTTTGTGTTCT 35
QY 2613 CTATTGATCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2646
DB 34 CTATTGATCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1

RESULT 3
AV522233/c 573 bp mRNA linear EST 01-SEP-2000
LOCUS
AV522233

DEFINITION	AV522233 Arabidopsis thaliana aboveground organs two to six-week old Arabidopsis thaliana CDNA clone Ap275C03F 3', mRNA sequence.
ACCESSION	AV522233
VERSION	AV522233.1
KEYWORDS	EST.
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	1 (bases 1 to 573) Asamizu, E., Nakamura, Y., Sato, S. and Tsubata, S.
TITLE	A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
JOURNAL	DNA Res. 7, 175-180 (2000)
MEDLINE	20363093
COMMENT	Contact: Erika Asamizu The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/. Location/Qualifiers
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DB	573 CAACACCTTCCTCTACTCTCCGACCGCAAAACCAATGAAATCAAGTTCCTCTT 514
0Y	2074 CCGATCTGTCCAGCCATACATCCCGGACATACAGCTCGCTTGAGCATTTTCTTCC 2133
DB	513 CCGATCTGTCCAGCCATACATCCCGGACATACAGCTCGCTTGAGCATTTTCTTCC 454
0Y	2134 ACGGGCAAGCAAACTACTGCTTGAAGAGCTCAAAACAACTAGGCTGAGTGAAGGA 2193
DB	453 ACGGGCAAGCAAACTACTGCTTGAAGAGCTCAAAACAACTAGGCTGAGTGAAGGA 394
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DB	393 ATATGAGAGCTTCTAGATGATGACACTTCAAGCTTGGAAACACTTATGACAGTGAATCT 334
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DB	273 AGATGCGTTTGGCTCTGCTGTTTAAAGTGAACAGTGTGTGGGAAGCAATAGAGGAAG 214
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DB	153 TCTAAATATATCATCTTCTTAAATTAATATCAAGTAAAGATCTCTAATTTACTCCAAAG 94

OY	2494	ATACGTTGGTGGAGTAGATAGAGACTTTATTACAGCATCAATGCATCTTAATCGTGTTA	2553
DB	93	ATACGTTGGTGGAGTAGATAGAGACTTTATTACAGCATCAATGCATCTGTATTATA	34
OY	2554	AGAATGATGTGGCTAGAGAGTCCTGTCCAGCTTC	2586
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DEFINITION		Old Arabidopsis thaliana cDNA clone APZL43B02R 5', mRNA sequence.	
ACCESSION		AV529660	
VERSION		AV529660.1 GI:8689943	
KEYWORDS		EST.	
SOURCE		thale cress.	
ORGANISM		Arabidopsis thaliana	
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
		Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;	
		Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
REFERENCE		Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.	
AUTHORS		A large scale analysis of cDNA in Arabidopsis thaliana: Generation	
TITLE		of 12,028 non-redundant expressed sequence tags from normalized and	
		size-selected cDNA libraries	
		DNA Res. 7, 175-180 (2000)	
JOURNAL		20363093	
MEDLINE		Contact: Erika Asamizu	
COMMENT		The First Laboratory for Plant Gene Research	
		Kazusa DNA Research Institute	
		Yana 1532-3, Kisarazu, Chiba 292-0812, Japan	
		Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.	
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		XhoI"	
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Best Local Similarity		100.0%; Pred. No. 9.9e-80;	
Matches 544: Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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DB	544	GCGCTCTAGAGATGACATCTCACAGSTTTGGAAACACTTCTAGACATGGAATCTGTATGA	485
OY	2261	GTTGCTTACATGAGGCCAAGAAAGTTCGTGAGAGCGATAGGTTTGGCAGATCGC	2320
DB	484	GTTGCTTACATGAGGCCAAGAAAGTTCGTGAGAGCGATAGGTTTGGCAGATCGC	425
OY	2321	TTTGGTCTGGTTTAAAGTGTAAAGTGTGGTGGGAAGCAAGAGAGAGTGAACA	2380
DB	424	TTTTGGTCTGGTTTAAAGTGTAAAGTGTGGTGGGAAGCAAGAGAGAGTGAACA	365
OY	2381	GCCAACGAGAACATCCCTGGTGGATGGCATCAACCGTTACCCTGGCCCTCTTAAT	2440
DB	364	GCCAACGAGAACATCCCTGGTGGATGGCATCAACCGTTACCCTGGCCCTCTTAAT	305
OY	2441	TATCATCTCTTAATTAATCAAGTAAATCTTAATTAATCTCAACCAAAAGATACGT	2500
DB	304	TATCATCTCTCTTAATTAATCAAGTAAATCTTAATTAATCTCAACCAAAAGATACGT	245

QY	2501	TTGGTTGGATGATGAGAGATTTATTTCTATCATCATGCTATGCTGTTATAAGAAATGG	2560
Db	244	TTGGTTGGATGATGAGAGATTTATTTCTATCATCATGCTATGCTGTTATAAGAAATGG	185
QY	2561	ATGTGGCTAGAGTCCGTGTTCAAGCTTGTTTATTTTGTGTTGTCCTATTTGGA	2620
Db	184	ATGTGGCTAGAGTCCGTGTTCAAGCTTGTTTATTTTGTGTTGTCCTATTTGGA	125
QY	2621	TCTTCATTAACCTTGAGAGATTTAAAGAAAAAAACCTCTCTTACGTTGATAGAAACAGATG	2680
Db	124	TCTTCATTAACCTTGAGAGATTTAAAGAAAAAAACCTCTCTTACGTTGATAGAAACAGATG	65
QY	2681	GTCATTTGTAATTTCTTTATAATGTCAAAGTAAGAACATTTCTTTTAAAGGCATCTATAT	2740
Db	64	GTCATTTGTAATTTCTTTATAATGTCAAAGTAAGAACATTTCTTTTAAAGGCATCTATAT	5
QY	2741	TCAG	2744
Db	4	TCAG	1

RESULT 5							
AV560055/c							
LOCUS	AV560055	526 bp	mRNA	linear	EST 07-SEP-2000		
DEFINITION	AV560055	Arabidopsis thaliana green siliques	Columbia	Arabidopsis thaliana	cdna clone	SO128c08f 3'	mRNA sequence.

VERSION	AV5560055.1	GI:8731481
KEYWORDS	EST.	
SOURCE	thale cress.	
ORGANISM	Arabidopsis thaliana	

REFERENCE
1 (bases 1 to 526)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

AUTHORs
 ASHIMIZU, E., NAKAMURA, I., SAKO, S. and IAKOTA, S.
 TITLE
 A large scale analysis of cDNA in *Arabidopsis thaliana*: Generation
 of 12,028 non-redundant expressed sequence tags from normalized and
 size-selected cDNA libraries
 JOURNAL
 DNA Res. 7, 175-180 (2000)

MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute

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FEATURES
source
    Location/Qualifiers
    1..526
    /orcnism="Arabidopsis thaliana"
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/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="SQ128C08F"
/clone_1["Arabidopsis thaliana green etiolated Columbia"]

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/tissue_type="green siliques"
/note="Vector: palunescriptII SK-; Site_1: ECORI; Site_2:
XhoI"
BASE COUNT      179 a       80 g       150 t
                   117 c

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Query Match	18.9%	Score 526;	DB 10;	Length 526;
Best Local Similarity	100.0%	Pred. No. 9e-77;		
Matches 526;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 2201 GGCCTTCAGGATGACACCTTCACAGGTTGGAAACCTTCAGCACTGGATGCA 2260
|||||
Db 526 GGCCTTCAGGATGACACCTTCACAGGTTGGAAACCTTCAGCACTGGATGCA 467

YY	TTTGGCGCTGTCGCTGTGTTAAACCTATTAAGCAGCCTGCTGCAACGCAG	2390
DY	2261 GTTGCCCTTACATTGGAGGCCAAGGAAGCTTCTGTAGAGCCATTAGGGCTTGGCAATGCG	2320
DB	466 GTTGCTTACATGAGGSCCAAAGAAAGCTTCGTAGAGGCCGATAGGGTTTGGCAATGCG	407

Db	406	TTTCGGTTCCTGGTTTTTAAGTGTAAACAGCTGCGTGTGGAAAGCAATGAGAAAGCTGAAGA	347
Qy	2381	GCCAACCCAGGAACAATCCCTGGGGGATTCATCAACCGTACCGCTGTCTAAAT	2440
Db	346	GCCAAACAGAGAACATTCCTGGTGGATTCGATCAACCGTTACCGTGTCTCTAAAT	287
Qy	2441	TATCATTTCTTCTAATTAATTAATCAATAGATCTCTAATTACTCCAAACCAAAAGATACAGT	2500
Db	286	TATCATTTCTTCTAATTAATTAATCAATAGATCTCTAATTAATCAACCAAAAGATACAGT	227
Qy	2501	TGGGTTGGATGTATAGAGATTTATTTACTGATCATTTGGTATCTAAGCTGTATTAAGAATGG	2560
Db	226	TTCGGTTGGATGTATAGAGATTTATTTACTGATCATTTGGTATCTAAGCTGTATTAAGAATGG	167
Qy	2561	ATGTGGCTAAGATCCCTGGTTCACGCTTCAACTGTTTATTTTGTGTGTTCTCTATTGGA	2620
Db	166	ATGTGGCTAAGATCCCTGGTTCACGCTTCAACTGTTTATTTTGTGTGTTCTCTATTGGA	107
Qy	2621	TCTTCATAAAGCTTTAGAGATTAAGAAAGAAAAAAGCTCTTCTTAGTTGATAGACAGATG	2680
Db	106	TCTTCATAAAGCTTTAGAGATTAAGAAAGAAAAAAGCTCTTCTTAGTTGATAGACAGATG	47
Qy	2681	GTCATTGTATTTCTTTAATATGTCAAAGTAAGAAATTTCTTTTT	2726
Db	46	GTCATTGTATTTCTTTAATATGTCAAAGTAAGAAATTTCTTTTT	1

RESULT 6	LOCUS	DEFINITION	504 bp	AV566012	Arabidopsis thaliana green siliques Columbia	EST 07-SEP-2000
AV566012/c	AV566012	Arabidopsis thaliana green siliques Columbia	504 bp	AV566012	Arabidopsis thaliana green siliques Columbia	EST 07-SEP-2000

thaliana cDNA clone SQ235a01F 3', mRNA sequence.	
ACCESSION	AY566012
VERSION	AY566012.1
KEYWORDS	GI:8737462
EST.	

ORGANISM	SOURCE
Arabiadopsis thaliana	thale cress.
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi	

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 504)	Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.	A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and

JOURNAL
MEDLINE
COMMENT

size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
20363093
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research

the first laboratory for plant virus research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamiu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>
asamiu@kazusa.or.jp

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1. 504
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"

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/cione_lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/note="Vector: pBluescriptII SK-, Site_1: EcoRI, Site_2:
XhoI"

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BASE COUNT	129 d	125 c	119	143 e
ORIGIN				
Query Match	18.1%	Score 504;	DB 10;	Length 504;
Best Local Similarity	100.0%	Prod No	3 7e-73.	

[illegible]

	Best Local Similarity	86.7%	Pred. No. 1,le-71;	
	Matches 556;	Conservative 0;	Mismatches 84;	Indels 1; Gaps 1;
QY 1118	GGTGCAGAAAGAAAGGTTCTATAGACTAGCGACGAAATATCAGAGGAGTTCGACGAGAGAGAC	1177		
Db 746	GGTGACAGAGAAAGAGATTTCATAGATCTAGCTAGAGAAATCA-GGCAGTTCGACGAGAGAGAT	688		
QY 1178	ACTGGGTTTCAGAGAAGAGGATCTTACAAAGCCTCAGGCGATGAGGCGACGAGACATACGTCC	1237		
Db 687	CCTGCATTTTCAGAAAAGAGATCTTCAAGCCCTCAGGATTAAGGCGATGAAGAGTACGTCC	628		
QY 1238	AAGATCCATCTCTTCATAGAAAACATATCAACAGCATGAAAGGTGCTGAAGAGCTC	1297		
Db 627	AAGATCAATCTCTTCGTCGGAAACACAAACAGATGAAGAGGTCTGAAAGAGCTC	568		
QY 1298	TACACTGATCTTTGGAGCAGTCAGACGACTCTTGGAGAAAGACAGTGTAAAACTBAAGA	1357		
Db 567	GATGATGATATTCGCGCAGCTCGACGAACTCTTGGAGAGACAGCTGTCAAAACCGAANA	508		
QY 1358	CGTTGGTCTCTTGTGTGTTAACTGTAGCATTTTCAACCCGACACCGTCTGTCCGCAT	1417		
Db 507	CGTAGTCTCTCGTGGTGTAACTGCAATCTTTAAACCGACCTCCGATCTCCGCAT	448		
QY 1418	GGTGATTAACCATTTCAAGATGAGAGGGAACATCTTATGTTACAACTTGGAGGATGG	1477		
Db 447	GGTGTATTAACCACTAACAAGATGAGGGGAACATCTTATGCTACAACTGAGAGGAGATGG	388		
QY 1478	ATGTTCCGCTGGAATCATAGCATATTTGATCTGCTCGTACACAGCTTCAGTCTAACCCCTAA	1537		
Db 387	TTGCTCAGCAGAGATCATAGCCGTTGATCTTCTGCTGATCTTACATGCTTACATACCGGA	328		
QY 1538	TAGTTATGCTCTTGTGTGTGAGTACTAGATGTTGGGTATATTTGTTAGTACGTGGGAAGTGA	1597		
Db 327	TAGTTACCGGATGGTGTGTGAGTACGAGATGTTGGGTATATTTGTTAGTACGTGGGACGTGA	268		
QY 1598	CAGTCATATGTTATTAACCTAATTTGTTTATAGATGGGTTGTCTGCCGTTATGCTTC	1657		
Db 267	CAGTCATATGTTATTAACCTAACCTGCTTTTATAGATGGGTTGTCTGCCGTTATGCTTC	208		
QY 1658	TAAAGCTGCTGTCGCTTCCGATGCTTAAGTACGCTTCGACGACATTTGCCGAACTCA	1717		
Db 207	TAAAGCTGCTGTCGCTTCCGATGCTTAAGTACGCTTCGACGACATTTGCCGAACTCA	148		
QY 1718	TAAAGCTGCTGACGACGCTAGCTTCAGGTTTCATTTATTTT	1758		
Db 147	CAAGGCTGCGCAGCACGCTAGCTTCAGGTTTCATTTATTT	107		
RESULT 8				
AV828119	585 bp	mRNA	linear	EST 01-APR-2002
LOCUS	AV828119			
DEFINITION	AV828119 RAFL9 Arabidopsis thaliana cDNA clone RAFL9-24-C03 5',			
ACCESSION	AV828119			
VERSION	AV828119.1			
KEYWORDS	EST.			
SOURCE	thale cress.			
ORGANISM	Arabidopsis thaliana			
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots;			
	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.			
	1 (bases 1 to 585)			
	Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,			
	Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,			
	Arakawa,T., Shibata,K., Shingawa,A., Muramatsu,M., Hayashizaki,Y.,			
	and Shinzaki,K.			
	Large scale analysis of Arabidopsis full-length cDNA (2002b)			
	Unpublished (2002)			
	Contact: Motoaki Seki			
	Plant Functional Genomics Research Group			
	RIKEN Genomic Sciences Center			
	3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan			
	Tel.: 81-298-36-4359			

Fax: 81-298-36-9060

Email: msekierc@riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified lambda phage-1 vector (Carlini et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pluscript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

source

Location/Qualifiers

1..585

/organism="Arabidopsis thaliana"

/db_xref="taxon:3702"

/clone="RAF109-24-C03"

/clone_1lb="RAF19"

/dev_stage="plants at various developmental stages from germination to mature seeds"

/lab_host="DH108"

/note="Site 1: BamHI; Site 2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"

BASE COUNT

161 a

130 c

128 g

165 t

1 others

ORIGIN

Query Match

Best Local Similarity

Matches 507; Conservative

0; Mismatches

24; Indels

0; Gaps

0;

17.7%; Score 493.2; DB 10; Length 585;

Pred. No. 2.1e-71;

Indels 0; Gaps 0;

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SOURCE

ORGANISM

Arabidopsis thaliana

REFERENCE

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thale cress.

Arabidopsis thaliana

Ekaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 710)

Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakaigima, M.,

Oono, Y., Sakurai, T., Carlini, P., Kawai, J., Itoh, M., Ishii, Y.,

Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.,

and Shinozaki, K.

Large scale analysis of Arabidopsis full-length cDNA (2002b)

Unpublished (2002)

Contact: Motoaki Seki

Plant Functional Genomics Research Group

RIKEN Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359

Fax: 81-298-36-9060

Email: msekierc@riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially

as reported previously (Seki et al., 1998). This clone is in a

modified pluscript vector as a SalI/XhoI insert. Please visit our

web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for

further details.

Location/Qualifiers

1..710

/organism="Arabidopsis thaliana"

/db_xref="taxon:3702"

/clone="RAF102-03-L07"

/clone_1lb="RAF12"

/dev_stage="rosette plants"

/lab_host="SOLR"

/note="Site 1: SalI; Site 2: XhoI"

BASE COUNT

206 a

159 c

156 g

187 t

2 others

ORIGIN

Query Match

Best Local Similarity

Matches 501; Conservative

0; Mismatches

13; Indels

0; Gaps

0;

17.7%; Score 493.2; DB 10; Length 710;

Pred. No. 1.9e-71;

Indels 0; Gaps 0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

Db 482 ATGAACACAAGGTGACAAAGACAGCTCATAGA 515
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RESULT 10
AV560773/c 474 bp mRNA linear EST 07-SEP-2000
AV560773 Arabidopsis thaliana green siliques Columbia Arabidopsis
DEFINITION
thaliana cDNA clone S014007F 3', mRNA sequence.
ACCESSION
AV560773
VERSION
AV560773.1 GI:8732199
KEYWORDS
EST.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 474)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
JOURNAL
MEDLINE
20363093
COMMENT
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
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Location/Qualifiers
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="S014007F"
/tissue_type="green siliques"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
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Best Local Similarity 100.0%; Pred. No. 3.2e-68;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 474 TATGAGGCTTCTAGATGACACTTTCACAGTTGGAAACCTCTACAGTGCATCTG 415
OY 2255 GTATGAGTTGGCTTACATGAGGCCAAGAAAGTTCGTAGAGCGATAGGTTGGCA 2314
|||||
Db 414 GTATGAGTTGGCTTACATGAGGCCAAGAAAGTTCGTAGAGCGATAGGTTGGCA 355
OY 2315 GATGCTTTGCGTTCTGCTTTAAAGTGAACAGTGTGTGGAAGCGCAATGAGAAAGT 2374
|||||
Db 354 GATGCTTTGCGTTCTGCTTTAAAGTGAACAGTGTGTGGAAGCGCAATGAGAAAGT 295
OY 2375 GAAGAAGCAACGAGAAACAATCCTGGGGTGGATTGCATCAACCGTTGCCCTCT 2434
|||||
Db 294 GAAGAAGCAACGAGAAACAATCCTGGGGTGGATTGCATCAACCGTTGCCCTCT 235
OY 2435 CTAATATATCATCTTCTTAATTAATCAAGTAAGATCTCAATTAATCAACCAAGA 2494
|||||
Db 234 CTAATATATCATCTTCTTAATTAATCAAGTAAGATCTCAATTAATCAACCAAGA 175
OY 2495 TACAGTTGGTTGGATGATGAGAGTATTTACGATCAATCGATCAATCGTTATTA 2554
|||||
Db 174 TACAGTTGGTTGGATGATGAGAGTATTTACGATCAATCGATCAATCGTTATTA 115
OY 2555 GAATGATGATGCTAGAGTCTGTTCAAGCTCAACCTGTTATTTTGGTTGCTCT 2614
|||||
Db 114 GAATGATGATGCTAGAGTCTGTTCAAGCTCAACCTGTTATTTTGGTTGCTCT 55

OY 2615 ATTGATCTCATTAACCTTGGAGATTAAGAAAAAAGCTCTCTTAGTTG 2668
|||||
Db 54 ATTGATCTCATTAACCTTGGAGATTAAGAAAAAAGCTCTCTTAGTTG 1
RESULT 11
AV564080/c 474 bp mRNA linear EST 07-SEP-2000
AV564080 Arabidopsis thaliana green siliques Columbia Arabidopsis
DEFINITION
thaliana cDNA clone S019810ZF 3', mRNA sequence.
ACCESSION
AV564080
VERSION
AV564080.1 GI:8735506
KEYWORDS
EST.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 474)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
JOURNAL
MEDLINE
20363093
COMMENT
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
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1. .474
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="S019810ZF"
/tissue_type="green siliques"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 164 a 104 c 70 g 136 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.2e-68;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2252 CTGATAGTGGCTTACATGAGGCCAAGAAAGTTCGTAGAGCGATAGGTTGG 2311
|||||
Db 474 CTGATAGTGGCTTACATGAGGCCAAGAAAGTTCGTAGAGCGATAGGTTGG 415
OY 2312 GCAATGCCCTTTCGTTCTGTTTAAAGTGAACAGTGTGTGGAAGCGCAATGAGAA 2371
|||||
Db 414 GCAGATCCCTTTCGTTCTGTTTAAAGTGAACAGTGTGTGGAAGCGCAATGAGAA 355
OY 2372 GGTGAAGAAGCAACGAGAAACAATCCTGGGTGATTCATCAACCGTTACCTGTGCC 2431
|||||
Db 354 GGTGAAGAAGCAACGAGAAACAATCCTGGGTGATTCATCAACCGTTACCTGTGCC 295
OY 2432 TCTCTAATATCATCTTCTTAATTAATCAAGTAAGATCTCAATTAATCAACCA 2491
|||||
Db 294 TCTCTAATATCATCTTCTTAATTAATCAAGTAAGATCTCAATTAATCAACCA 235
OY 2492 AGATCAATTTGGTTGGATGATGAGAGTATTTACGATCAATCGATCAATCGTTATTA 2551
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Db 234 AGATCAATTTGGTTGGATGATGAGAGTATTTACGATCAATCGATCAATCGTTATTA 175
OY 2552 TAAGATGATGATGCTAGAGTCTGTTCAAGCTCAACCTGTTATTTTGGTTGCTC 2611
|||||
Db 174 TAAGATGATGATGCTAGAGTCTGTTCAAGCTCAACCTGTTATTTTGGTTGCTC 115
OY 2612 TCTATGATCTTCATTAACCTTGGAGATTAAGAAAAAAGCTCTCTTAGTTGATA 2671

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|||||
Db 114 TCTATTGATCTTCATTAACCTTGAGAGATTAAAGAAAAAACTCTTCTTGTAGTTGATTA 55
Oy 2672 GAACAGATGTCATTTCTTAATTTCTTAATATGCAAGTAACAACTTTCTTT 2725
Db 54 GACACAGATGTCATTTCTTAATTTCTTAATATGTCACAAAGTAACAACTTTCTTT 1

RESULT 12
AV563747/c 462 bp mRNA linear EST 07-SEP-2000
LOCUS AV563747
DEFINITION Arabidopsis thaliana green siliques Columbia Arabidopsis
Chailana cDNA clone SQ192e10f 3', mRNA sequence.
ACCESSION AV563747
VERSION AV563747.1 GI:8735173
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 462)
REFERENCE Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yama 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
source
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/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="SQ192e10f"
/clone.lib="Arabidopsis thaliana green siliques Columbia"
/tissue.type="green siliques"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 158 a 99 c 69 g 136 t
ORIGIN
Query Match 16.5%; Score 460.4; DB 10; Length 462;
Best Local Similarity 99.8%; Pred. No. 5.5e-66;
Matches 461; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2269 ACATGAGGCCAAGAAAGTTCGTAGAGGCGATAGGGTTGGCAGATCGCTTTCGTT 2328
Db 462 ACATGAGGCCAAGAAAGTTCGTAGAGGCGATAGGGTTGGCAGATCGCTTTCGTT 403
Oy 2329 CTGGTTTAAAGTGAACATGTGGTGTGAAGCAATGGAAGTGAAGAACCAACCA 2388
Db 402 CTGGTTTAAAGTGAACATGTGGTGTGAAGCAATGGAAGTGAAGAACCAACCA 343
Oy 2389 GGAACAATCCCTGGGTGATGCATCAACCGTTACCGCTGCTCTTAATATCATTC 2448
Db 342 GGAACAATCCCTGGGTGATGCATCAACCGTTACCGCTGCTCTTAATATCATTC 283
Oy 2449 TTCTAAATTAATCAAGTAAGATCTCTAATTAATCTCCAAACCAAGATACAGTTGGTGG 2508
Db 282 TTCTAAATTAATCAAGTAAGATCTCTAATTAATCTCCAAACCAAGATACAGTTGGTGG 223
Oy 2509 ATGATAGAGGATATTACTGATCATTCGTATCAAGCTGTATTAAGAAATGATGTGGCT 2568
Db 222 ATGATAGAGGATATTACTGATCATTCGTATCAAGCTGTATTAAGAAATGATGTGGCT 163
Oy 2569 AAGAGTCCTGAGCTCAACTGTTTATTTTGTGTGTCTCTATATGATGATCTTCATA 2628
Db 162 AAGAGTCCTGAGCTCAACTGTTTATTTTGTGTGTCTCTATATGATGATCTTCATA 103

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Oy 2629 AACTTGAGAGATTAAGAAAAAACTCTTCTTACTTGTATGATGAACAGATGTCATTC 2688
Db 102 AACTTGAGAGATTAAGAAAAAACTCTTCTTACTTGTATGATGAACAGATGTCATTC 43
Oy 2689 AATTCTTAATATGTCACAAAGTAACAACTTTCTTTAAG 2730
Db 42 AATTCTTAATATGTCACAAAGTAACAACTTTCTTTAAG 1

RESULT 13
AV797399/c 453 bp mRNA linear EST 29-MAR-2002
LOCUS AV797399
DEFINITION Arabidopsis thaliana cDNA clone RAFL09-11-P14 3',
mRNA sequence.
ACCESSION AV797399
VERSION AV797399.1 GI:19831382
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 453)
REFERENCE Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.,
and Shinohara, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified lambda phiC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.
FEATURES
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Db 393 GTCTAACACTGTGTGTGAAGCAATGAGAGTGAAGAACCAACCAAGACATCC 334
Oy 2399 TTGGGTGATGTCATCAACCGTTACCGCTGCTCTTAATATCATTCCTTAATTA 2458

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Db 213 TTATGATGATCATCTGATCTAAGTCTGTATTAAGAAGATGAGTGGCTAGTCTGT 154

QY 2579 TCACCTTCACCTGTTTATTTTGTGTTGTTCTATGATCTTCATTAACCTTGAGA 2638

Db 153 TCACCTTCACCTGTTTATTTTGTGTTGTTCTATGATCTTCATTAACCTTGAGA 94

QY 2639 GATTAAGAAAAAAACCTCTCTTGTAGTTGATAGAACAGATGATCATTAATTTCTTA 2698

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DEFINITION thaliana cDNA clone SQ189h10f 3', mRNA sequence.

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VERSION AV563591.1 GI:8735017
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

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QY 2314 AGATCGCTTGGCTTGGCTTTAAGTGTACAGTGTGGTGTGAGAGCAATGAGGAAG 2373

Db 413 AGATCGCTTGGCTTGGCTTTAAGTGTACAGTGTGGTGTGAGAGCAATGAGGAAG 354

QY 2374 TGAAGAACCAACGAGCAATCCTTGGTGATGATCAACCGTTACCTGTGCTC 2433

Db 353 TGAAGAACCAACGAGCAATCCTTGGTGATGATGATCAACCGTTACCTGTGCTC 294

QY 2434 TCTAATATCATCTTCTTAATTAATCACTAAGATCTCTAATTTACTCCACCAAAAG 2493

Db 233 TCTAATATCATCTTCTTAATTAATCACTAAGATCTCTAATTTACTCCACCAAAAC 234

QY 2434 ATACGTTGGTGGATGATGAGTATTTATTCATATTCGATATTCGATGCTTATA 2553

Db 233 ATACGTTGGTGGATGATGAGTATTTATTCATATTCGATATTCGATGCTTATA 174

QY 2554 AGAATGAGATGGCTAGAGTCCCTGTTCAAGCTTCAACTGTTTATTTTGTGCTGC 2613

Db 173 AGAATGAGATGGCTAGAGTCCCTGTTCAAGCTTCAACATGTTTATTCCTGTGTGCTGC 114

QY 2614 TATTGATCTTCATTAACCTTTGAGAGATTAAAGAAAAAAACCTCTTTAGTTGATAGA 2673

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DEFINITION thaliana cDNA clone FB004e01f 3', mRNA sequence.

ACCESSION AV530486
VERSION AV530486.1 GI:8690769
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

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BASE COUNT 157 a 91 c 65 g 130 t
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Best Local Similarity 99.8%; Pred. No. 7.4e-63;
Matches 442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 443 AAAGTGTGTAAGAGCGATAGGGTTTGGCAGATCGCTTGGCTTGTATGCTA 384

QY 2344 ACAGTGTGTCGAAGCAATGAGAGGTGCAAGCAACCAACGAGCAATCCTTGGG 2403

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Db 383 ACAGTGTGTTGGAGGCAATGAGAGAGTGAGAACCAACCAAGACAATCCTTGGG 324
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Db 323 TGGATTGCATCAACCGTTACCGTGGCTCTTAATTATCATTCCTTAATTAAATCA 264
QY 2464 AGTAGATCTCTAATTACTGCAACCAAGATACAGTTGGTTGGATGATAGAGTTATT 2523
Db 263 AGTAGATCTCTAATTACTGCAACCAAGATACAGTTGGTTGGATGATAGAGTTATT 204
QY 2524 TACTGATCATTCGATCTAGCTGTATTAAGAAATGATGGCTAGAGTCCGTGTCAGC 2583
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QY 2704 TCAAAGTAAACAATTCCTTTT 2726
Db 23 TCAAAGTAAACAATTCCTTTT 1
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Job time : 3505 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2003, 17:46:08 ; Search time 6984 Seconds
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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8	1412.4	50.8	1425	8 AF21449752	AF214498 Arabidops
9	1412.4	50.8	1425	8 AF21449952	AF214500 Arabidops
10	1412.4	50.8	1425	8 AF21450152	AF214502 Arabidops
11	1412.4	50.8	1425	8 AF21450352	AF214504 Arabidops
12	1412.4	50.8	1425	8 AF21450552	AF214506 Arabidops
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25	517.2	18.6	1903	8 AY072823	AY072823 Gossypium
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent EP1174517.
ACCESSION AX353344
VERSION AX353344.1 GI:18618426
KEYWORDS
SOURCE
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thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS
TITLE
1
Lechelt-Kunze,C., Meissner,R. and Tietjen,K.
Use of very long chain fatty acid elongase for the identification


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SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
AUTHORS 1 (bases 1 to 2782)
Yephremov A., Wismar, E., Hüljser, P., Hüljser, C., Wellesen, K. and
Saedler, H.
TITLE Characterization of the FIDDLEHEAD gene of Arabidopsis reveals a
link between adhesion response and cell differentiation in the
epidermis
JOURNAL Plant Cell 11 (11), 2187-2201 (1999)
MEDLINE 20025656
PubMed 10559443
REFERENCE 2 (bases 1 to 2782)
Yephremov, A.
AUTHORS Direct Submission
TITLE Submitted (27-AUG-1998) Yephremov A., Molekulare Pflanzen-genetik,
Max-Planck-Institut fuer Zuechtungs-forschung, Carl-von-Linne-Weg
10, Koeln D-50829, Germany
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Rounsley, S.D., Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C.,
Somerville, C.R., and Venter, J.C.
JOURNAL
2 (bases 1 to 82212)
Unpublished
AUTHORS Lin, X.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
REFERENCE
3 (bases 1 to 82212)
Town, C.D. and Kaul, S.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA, cdtown@tigr.org
COMMENT
On Apr 18, 2002 this sequence version replaced gi:5598423.
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Oy	1021	CGGACTGATTAATTAATTAATGACTGATTAATCAAAACCAAAAGTTTATTTAATTCGGTTC	1080
Dd	48053	CGGACTGATTAATTAATTAATGACTGATTAATCAAAACCAAAAGTTTATTTAATTCGGTTC	48112
Oy	1081	TCTCGGTTTAACTCTTTTTCATTTGATGATGTTTAACTGATGACAAAGAAGTTTCATAG	1140
Dd	48113	TCTCGGTTTAACTCTTTTTCATTTGATGATGTTTAACTGATGACAAAGAAGTTTCATAG	48172
Oy	1141	AACCTGCGAGAAATTCAGAGGAAGTTCGACGGAAGACACACTGGGTTTCAAGAAGAGATCT	1200
Dd	48173	AACCTGCGAGAAATTCAGAGGAAGTTCGACGGAAGACACACTGGGTTTCAAGAAGAGATCT	48232
Oy	1201	TACAAAGCTTCAGGCTATAGGCGCAGACATACAGTCCCAAGATCCATCTCTTCATCAGAA	1260
Dd	48233	TACAAAGCTTCAGGCTATAGGCGCAGACATACAGTCCCAAGATCCATCTCTTCATCAGAA	48292
Oy	1261	ACATACACAACGATGAAAAGAGTCTGTGAAGAAGCTCTTACAGTATCTTTGGACACTAG	1320
Dd	48293	ACATACACAACGATGAAAAGAGTCTGTGAAGAAGCTCTTACAGTATCTTTGGACACTAG	48352
Oy	1321	ACGAACCTTTCGAGAGACAGCTGTAAAAACCTTAAAGAGTTGGTCTCTTGCGGTTAACT	1380
Dd	48353	ACGAACCTTTCGAGAGACAGCTGTAAAAACCTTAAAGAGTTGGTCTCTTGCGGTTAACT	48412
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Dd	48413	GTAGCATTTTCAACCCGACACCGCTGTTGTCCGAAATGATGATAACATTTACAAGATGA	48472
Oy	1441	GAGGGAACATCTTGTGTTACCAACCTTGGAGGAGTGGAGTTCGGCTGGAAATCATAGCTA	1500
Dd	48473	GAGGGAACATCTTGTGTTACCAACCTTGGAGGAGTGGAGTTCGGCTGGAAATCATAGCTA	48532
Oy	1501	TTGATCTTGCTCGTGACATGCTCTACGTAAACCTTAATAGTTATGCTGTGTTGAGTA	1560
Dd	48533	TTGATCTTGCTCGTGACATGCTCTACGTAAACCTTAATAGTTATGCTGTGTTGAGTA	48592
Oy	1561	CTGAGATGTTGGGTATTAATTTGTACGTGGGAGTGAACAAGTCAATGGTTATACCTAAT	1620
Dd	48593	CTGAGATGTTGGGTATTAATTTGTACGTGGGAGTGAACAAGTCAATGGTTATACCTAAT	48652
Oy	1621	GTTTTGTAGAGTGGGTGTTCTCGCCGTTATGCTCTCAACCGCTGCTGACTTTCGCC	1680
Dd	48653	GTTTTGTAGAGTGGGTGTTCTCGCCGTTATGCTCTCAACCGCTGCTGACTTTCGCC	48712
Oy	1681	ATGCTAAGTACCGTCTGAGCACATTTGTCGGAATCATPAAGGCTGCTGACGACGTAGCT	1740
Dd	48713	ATGCTAAGTACCGTCTGAGCACATTTGTCGGAATCATPAAGGCTGCTGACGACGTAGCT	48772
Oy	1741	TCAGGTTTCATTCATTTTGGATTAATTAATCGTTTACATTCCTTACAGCACTAATACT	1800
Dd	48773	TCAGGTTTCATTCATTTTGGATTAATTAATCGTTTACATTCCTTACAGCACTAATACT	48831
Oy	1801	AATTTTGTGTGTTTTTGAAGAGTGTGTACCAAGGAAGATGTAACAAGATTCAAGGGGT	1860
Dd	48832	AATTTTGTGTGTTTTTGAAGAGTGTGTACCAAGGAAGATGTAACAAGATTCAAGGGGT	48891
Oy	1861	TGAAGATATGTAAGACACTTAATGGAAGTTTGAAGGTGAAGCTCTCAAGACAAACATCACTA	1920
Dd	48892	TGAAGATATGTAAGACACTTAATGGAAGTTTGAAGGTGAAGCTCTCAAGACAAACATCACTA	48951

[illegible]

RESULT 4	AF21448952	AF21448952	1425 bp	DNA	linear	PLN 17-MAY-2000
LOCUS	AF21448952	Arabidopsis thaliana cultivar Landsberg	erecta fiddlehead protein			
DEFINITION	Arabidopsis thaliana cultivar Landsberg	(fhd) gene, complete cds.				
ACCESSION	AF214490					
VERSION	AF214490.1	GI:8177698				
KEYWORDS						
SEGMENT						
SOURCE						
ORGANISM						

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi-
s.
1 (bases 1 to 1425)
Pruitt, R.E., Vielle-Calzada, J.P., Ploense, S.E., Grossniklaus, U. and
Lolle, S.J.
FIDDLEHEAD, a gene required to suppress epidermal cell interactions
in Arabidopsis, encodes a putative lipid biosynthetic enzyme
Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)
MEDLINE
20122614
PUBMED
10655527
2 (bases 1 to 1425)
Pruitt, R.E., Vielle-Calzada, J.P., Ploense, S.E., Grossniklaus, U.
and Lolle, S.J.
Direct Submission
Submitted (13-DEC-1999) Molecular and Cellular Biology, Harvard
University, 16 Divinity Avenue, Cambridge, MA 02138, USA
FEATURES
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BASE COUNT 396 a 294 c 335 g 400 t
ORIGIN
Query Match 50.88; Score 1414; DB 8; Length 1425;
Best Local Similarity 99.98; Pred. No. 6.2e-251;
Matches 1425; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Db 361 AGGATGGGATGTTGGCTGGATCATATGATGATCTTCGTCGATGCTTCAGTC 420
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Db 541 TATGCTCTTAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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Db 661 CGTTTACATCTCTTGA-CGACCTAGTAACTAATTTTGTGTTTATAGAGTGTGTA 719
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Db 780 TGAAGTGAAGCTCTCAAGACAAATCATTACTTAACTGCTCTTCTTCTTCTC 839
QY 1949 CGACAGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2008
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Db 840 CGACAGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
QY 2009 GTCCACAACCT 2068
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Db 1200 TTGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1259
QY 2369 GAAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2428
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RESULT 5
AF214491S2 1425 bp DNA linear PLN 17-MAY-2000
LOCUS Arabidopsis thaliana fiddlehead protein (fdh) gene, fdh-1 allele,
DEFINITION complete cds.
ACCESSION AF214492
VERSION AF214492.1 GI:8177702
KEYWORDS 2 of 2
SEGMENT Arabidopsis thaliana.
SOURCE Arabidopsis thaliana.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1425)
Pruitt, R.E., Yelle-Calzada, J.P., Ploense, S.E., Grossniklaus, U. and
Lolle, S.J.
FIDDLEHEAD, a gene required to suppress epidermal cell interactions
in Arabidopsis, encodes a putative lipid biosynthetic enzyme
Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)
20122614
2 (bases 1 to 1425)
Pruitt, R.E., Yelle-Calzada, J.P., Ploense, S.E., Grossniklaus, U.
and Lolle, S.J.
Direct Submission
Submitted (13-DEC-1999) Molecular and Cellular Biology, Harvard
University, 16 Divinity Avenue, Cambridge, MA 02138, USA
Location/Qualifiers
1. 1425
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/db_xref="taxon:3702"
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/note="FIDDLEHEAD"
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BASE COUNT 397 a 294 c 334 g 400 t
ORIGIN
Query Match 50.8%; Score 1412.4; DB 8; Length 1425;
Best Local Similarity Pred. No. 1.2e-250;
Matches 1424; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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DB 1 ATGGTTTAGTGACAAAGAGGTTTCATAGAACTAGCGAGAAACAGGAAAGTTCGA 60
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DB 541 TATGCTCTTAACCGTGTGTGCTGCTTTCGCCATGTAAGTACCGTCTCGACGACATTTGT 600
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DB 661 CGTTTTCATCTCTTACCGACCTAGTAACTAATTTGTGTGTTTAAAGAGTGTGA 719
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DB 780 TGGAGTGAAGCTCTCAAGACAAACATCACTACCTTGTGTCCTTCTCTACCTTCTC 839
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Db 1380 AAAAGATACAGTTGGTGGATGATAGAGATTAATTAATCAATCTCTAATTAATCAAC 1425

RESULT 6
AF214493S2 1425 bp DNA linear PLN 17-MAY-2000
LOCUS Arabidopsis thaliana fiddlehead protein (fdh) gene, fdh-2 allele,
DEFINITION complete cds.
ACCESSION AF214494.1 GI:8177706
VERSION AF214494
KEYWORDS 2 of 2
SEGMENT Arabidopsis thaliana.
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 1425)
Pruitt,R.E., Vielle-Calzada,J.P., Ploense,S.E., Grossniklaus,U. and
Lolle,S.J.
FIDDLEHEAD, a gene required to suppress epidermal cell interactions
in Arabidopsis, encodes a putative lipid biosynthetic enzyme
Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)
20122614
PUBMED 10655527
REFERENCE 2 (bases 1 to 1425)
Pruitt,R.E., Vielle-Calzada,J.P., Ploense,S.E., Grossniklaus,U.
and Lolle,S.J.
Direct Submission
Submitted (13-DEC-1999) Molecular and Cellular Biology, Harvard
University, 16 Divinity Avenue, Cambridge, MA 02138, USA
FEATURES
source location/Qualifiers
1..1425
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
order(AF214493.1:1..656,1..1425)
/gene="fdh"
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BASE COUNT 397 a 294 c 334 g 400 t
ORIGIN

Query Match 50.8%; Score 1412.4; DB 8; Length 1425;
Best Local Similarity 99.9%; Pred. No. 1,2e-250;
Matches 1424; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1109 ATGGTTTAGTGACAAAGAGAGTTCAAGACAGTAGACGAGAAATCAGGAGATTGCA 1168
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Db 780 TGGAGGTGACCTGTCAGAACCAATCATACCTTAGGCTCTGTCCTGCTACCTTCTC 839
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LOCUS Arabidopsis thaliana fiddlehead protein (fdh) gene, fdh-5 allele,
DEFINITION complete cds.
ACCESSION AF214500
VERSION AF214500.1 GI:8177718
KEYWORDS 2 of 2
SEGMENT Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1425)
REFERENCE 1
AUTHORS Pruitt,R.E., Vielle-Calzada,J.-P., Ploense,S.E., Grossniklaus,U. and
Loile,S.J.
FIDDLEHEAD, a gene required to suppress epidermal cell interactions
in Arabidopsis, encodes a putative lipid biosynthetic enzyme
Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)
JOURNAL MEDLINE
PUBMED 10653527
2 (bases 1 to 1425)
REFERENCE 2
AUTHORS Pruitt,R.E., Vielle-Calzada,J.-P., Ploense,S.E., Grossniklaus,U.

and Loile,S.J.
Direct Submission
Submitted (13-DEC-1999) Molecular and Cellular Biology, Harvard
University, 16 Divinity Avenue, Cambridge, MA 02138, USA
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Best Local Similarity 99.9%; Pred. No. 1.2e-250;
Matches 1424; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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 DEFINITION complete cds.
 ACCESSION AF214502
 VERSION AF214502.1 GI:8177722
 KEYWORDS
 SEGMENT 2 of 2
 SOURCE Arabidopsis thaliana.

ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 1425)
 Pruitt,R.E., Vielle-Calzada,J.P., Ploense,S.E., Grossniklaus,U. and
 Lolle,S.J.
 FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 in Arabidopsis, encodes a putative lipid biosynthetic enzyme
 Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)
 20122614
 10655527
 2 (bases 1 to 1425)
 Pruitt,R.E., Vielle-Calzada,J.P., Ploense,S.E., Grossniklaus,U.
 and Lolle,S.J.
 Direct Submission
 Submitted (13-DEC-1999) Molecular and Cellular Biology, Harvard
 University, 16 Divinity Avenue, Cambridge, MA 02138, USA
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 BASE COUNT 397 a 294 c 334 g 400 t
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Query Match 50.8%; Score 1412.4; DB 8; Length 1425;
 Best Local Similarity 99.9%; Pred. No. 1.2e-250;
 Matches 1424; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Oy 1109 ATTGGTTAGTGAAGAGAGAGTTCATGACTGCGGAAATTCAGGAACTTGA 1168
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DEFINITION complete cds.
ACCESSION AF214504.1 GI:8177726
VERSION AF214504.1
KEYWORDS 2 of 2
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana.
REFERENCE 1. Fruitt, R.E., Velle-Calzada, J.F., Ploense, S.E., Grossniklaus, U. and Lolle, S.J. FIDDLEHEAD, a gene required to suppress epidermal cell interactions in Arabidopsis, encodes a putative lipid biosynthetic enzyme Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)
JOURNAL MEDLINE 20122614
PUBMED 10655527
REFERENCE 2. (bases 1 to 1425)
AUTHORS Fruitt, R.E., Velle-Calzada, J.F., Ploense, S.E., Grossniklaus, U. and Lolle, S.J.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-1999) Molecular and Cellular Biology, Harvard University, 16 Divinity Avenue, Cambridge, MA 02138, USA
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Query Match 50.8%; Score 1412.4; DB 8; Length 1425;
Best Local Similarity 99.9%; Pred. No. 1.2e-250;
Matches 1424; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Db 1109 ATTGGTTAGGTGACAAAGAGTGCATAGACTGCGGAGAAATCAGGAAAGTTCGA 1168
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1169 CGAAGACACTCGGTTTCAAGAGAGATCTTACAAGCCTCAGCAGTACGCGAGAG 1228

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 DEFINITION
 Arabidopsis thaliana fiddlehead protein (fdh) gene, fdh-9 allele,
 complete cds.
 ACCESSION
 AF214506
 VERSION
 AF214506.1 GI:8177730
 KEYWORDS
 SEGMENTS
 SOURCE
 ORGANISM
 Arabidopsis thaliana.
 Arabidopsis thaliana.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 1425)
 Pruitt,R.E., Viellet-Calzada,J.P., Ploense,S.E., Grossniklaus,U. and
 Lolle,S.J.
 FIDDLEHEAD, a gene required to suppress epidermal cell interactions
 in Arabidopsis, encodes a putative lipid biosynthetic enzyme
 Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1311-1316 (2000)
 20122614
 PUBMED
 10655527
 REFERENCE
 2 (bases 1 to 1425)
 Pruitt,R.E., Viellet-Calzada,J.P., Ploense,S.E., Grossniklaus,U.
 and Lolle,S.J.
 Direct Submission
 Submitted (13-DEC-1999) Molecular and Cellular Biology, Harvard
 University, 16 Divinity Avenue, Cambridge, MA 02138, USA
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 BASE COUNT 396 a 294 c 334 g 401 t
 ORIGIN

Query Match 50.8%; Score 1412.4; DB 8; Length 1425;
 Best Local Similarity 99.9%; Pred. No. 1.2e-250;
 Matches 1424; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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RESULT 13
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 DEFINITION Arabidopsis thaliana putative beta-ketoacyl-CoA synthase FIDDLEHEAD
 (At2g26250) mRNA, complete cds.
 ACCESSION AF337910
 VERSION AF337910.1 GI:12597466
 KEYWORDS FLI-CDNA.
 SOURCE Arabidopsis thaliana.
 ORGANISM Arabidopsis thaliana.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 1927)

REFERENCE
 AUTHORS Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
 Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
 Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
 Jones,T., Kamuya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
 Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
 Satou,M., Seki,M., Shimu,P., Southwick,A., Shinozaki,K.,
 Davis,R.W., Ecker,J.R. and Theologis,A.
 Arabidopsis Full Length cDNA Clones

TITLE
 JOURNAL Arabidopsis Full Length cDNA Clones
 REFERENCE
 AUTHORS Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
 Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
 Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
 Jones,T., Kamuya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
 Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
 Satou,M., Seki,M., Shimu,P., Southwick,A., Shinozaki,K.,
 Davis,R.W., Ecker,J.R. and Theologis,A.
 Arabidopsis Full Length cDNA Clones

TITLE
 JOURNAL Arabidopsis Full Length cDNA Clones
 REFERENCE
 AUTHORS Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
 Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
 Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
 Jones,T., Kamuya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
 Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
 Satou,M., Seki,M., Shimu,P., Southwick,A., Shinozaki,K.,
 Davis,R.W., Ecker,J.R. and Theologis,A.
 Arabidopsis Full Length cDNA Clones

COMMENT
 The Salik, Stanford, PGEC (SSP) Consortium members carried out the
 sequencing and annotation of the RFLV cDNAs: Yamada,K., Liu,S.X.,
 Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D.,
 Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Chen,H.,

The Salik, Stanford, PGEC (SSP) Consortium members carried out the
 sequencing and annotation of the RFLV cDNAs: Yamada,K., Liu,S.X.,
 Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D.,
 Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Chen,H.,

Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J.,
Miranda, M., Nguyen, M., Palm, C.J., Shim, P., Southwick, A.,
Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SSP/PGECC) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGECC)
contributed equally to this work as PIs.

FEATURES

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VLVNCISDEPTSLSAMVINHYKMRGNILSYNGMGCSAGIADLADMDLQSN

SYAVVSTEWGYNMYGSDKSMVIPCFFPMCSAVMLNRRRDFHAYRLEHIVR

THRAADRFSRYOEDEQGFGLKISRLMEFGALKTNTITLGLPVLVPEEOL

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1737. 1927

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543 t

ORIGIN

Query Match

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Matches 1422; Conservative 0; Mismatches 2; Indels 75; Gaps 1;

48.0%; Score 1335.8; DB 8; Length 1927;

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VERSION	AY039563.1	GI:14517455	
KEYWORDS	FLI_CDNA.		
SOURCE	Arabidopsis thaliana.		
ORGANISM	Arabidopsis thaliana.		
REFERENCE			
AUTHORS	Kim,C.J., Chen,H., Cheuk,R., Koesema,E., Meyers,M.C., Banh,J., Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.		
TITLE	Arabidopsis cDNA clones		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1911)		
AUTHORS	Kim,C.J., Chen,H., Cheuk,R., Koesema,E., Meyers,M.C., Banh,J., Bower,L., Carninci,P., Dale,J.M., Gibson,H.A., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-JUN-2001) Salk Institute Genomic Analysis Laboratory		
COMMENT	(Signal), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
	RIKEN Genomic Sciences Center (GSC) members carried out the collection and annotation of the RAFL cDNAs (RAFL_CDNA : 'RIKEN Arabidopsis Full-length cDNA' : Seki,M., Narusaka,M., Ishida,J., Saccu,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.		
	The Salk, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shin,P., Chen,H., Cheuk,R., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J., Bower,L., Dale,J.M., Gibson,H.A., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yu,G., Yu,S., Davis,R.W., Theologis,A. and Ecker,J.R.		
FEATURES			
source	Shinn,P. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIs.		
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DEFINITION Sequence 7 from patent US 6307128.
ACCESSION ARI174889
VERSION ARI174889.1 GI:17915209
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1650)
AUTHORS Jaworski,J.G., Post-Beltemiller,M.Ann. and Todd,J.
TITLE Fatty acid elongases
JOURNAL Patent: US 6307128-A 7 23-OCT-2001;
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source 1.1650
Location/Qualifiers
BASE COUNT 429 a 359 c 407 g 455 t
ORIGIN

Query Match 41.6%; Score 1157.4; DB 6; Length 1650;
Best Local Similarity 94.2%; Pred. No. 1.3e-203;
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 PR (FARB) BAYER AG.
 XX Lechelt-Kunze C, Meissner R, Thieljen K;
 PI WPI; 2002-156695/21.
 DR P-PSDB; AAM48794.
 XX Use of a polypeptide with very long chain fatty acid elongase activity
 PT for identifying herbicides, and of its nucleic acid for identifying
 PT specific modulators -
 PS Claim 9; Page 13-17; 22pp; German.
 XX
 CC The invention relates to use of a polypeptide with very long chain fatty
 CC acid elongase (VLCFAE) activity for identifying herbicides. The protein
 CC and the nucleic acid that encodes it, are used to identify compounds,
 CC including herbicides and plant-growth regulators, that alter activity or
 CC expression of the protein. The nucleic acid is also used to produce
 CC transgenic plants with altered activity or expression of the protein and
 CC for recombinant preparation of the protein. The invention relates
 CC especially to the fiddlehead (fdh) protein (GenBank Accession Number
 CC CA009311) and encoding DNA sequence (GenBank Accession Number AJ010713)
 CC isolated from the thale cress *Arabidopsis thaliana* and with VLCFAE
 CC activity.
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OY 1717 ATAAAGCTGCTGACGACCGTAGCTTCAAGTTTCACTTATTTGGTATTAFTGCTTTAC 1776
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Db 1074 ATAAAGCTGCTGACGACCGTAGCTTCAAGTTTCACTTATTTGGTATTAFTGCTTTAC 1099
OY 1777 AATCTCTTGACCGACCTAGTAACTAATTTGTTGAGAGTGTGTACGAGAG 1836
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Db 1119 AAGATGAACAAGATTCAGAGGGTTGAAGTAAGTAGAGACTTAATGGAAGTTGGAGGTG 1178
OY 1897 AAGCTCTCAAGACAACATCACTACCTTAGTGTCTTGTCTTACCTTCTCGAGAGC 1956
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OY 1957 TTCTCTTCTTGTGCTTGTGCTCGCGCAATCTCACCCTGTGCCAAAAGCTCCAAA 2016
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Db 1239 TTCTCTTCTTGTGCTTGTGCTCGCGCAATCTCACCCTGTGCCAAAAGCTCCAAA 1298
OY 2017 CCACCTTCCTTCTTACTCTCGCGCAACGCAAAAACCAATGGAATCAAGTCTTCTCCG 2076
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Db 1299 CCACCTTCCTTCTTACTCTCGCGCAACGCAAAAACCAATGGAATCAAGTCTTCTCCG 1358
OY 2077 ATCTGTCCAAGCATATCATCCGAGCTACAAAGCTCGCCTCGAGCAATTTTGGTCCAG 2136
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OY 2137 CGGCAAGCAAGATAGTGTGAAGAGCTTCAAAAGATCTAGGCTTGAAGAGATA 2196
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Db 1419 CGGCAAGCAAGATAGTGTCTTGAAGAGCTTCAAAAAGATCTAGGCTTGAAGAGATA 1478
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OY 2317 TCGCTTCGGTTCGTGTTTAAAGTGTAAACAGTGTGTGTGGAAGGCAATGAGAAAGTGA 2376
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OY 2677 GATGCTCATTTGTAATTTCTTAAATATGTCAAAGTAAACAATTTCTTTT 2726
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RESULT 3
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XX 17-OCT-2000 (first entry)
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XX Arabidopsis thaliana DNA fragment SEQ ID NO: 3549.
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XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
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PR 29-OCT-1999; 99US-0162142-

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Query Match 49.9%; Score 1388.4; DB 21; Length 1949;
 Best Local Similarity 95.1%; Pred. No. 1.8e-260;
 Matches 1474; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

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QY 1117 AGGTGACAAAGAGAGATCTTACAAAGCTCAGGCGAGAGATACGTC 1176
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QY 1177 CACTGCTTCAAGAGAGATCTTACAAAGCTCAGGCGAGAGATACGTC 1236
DB 534 CACTGCTTCAAGAGAGATCTTACAAAGCTCAGGCGAGAGATACGTC 593
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DB 594 CAAGTTCATCTCTTCATCAGAAAACATACAAAGATGAGAGAGATCT 653
QY 1297 CTACAGTGTCTTTGGAGACAGAGAGATCTTGGAGAGAGATCTTAA 1356
DB 654 CTACAGTGTCTTTGGAGACAGAGAGATCTTGGAGAGAGATCTTAA 713
QY 1357 AGCTGTGTCTTGTGTGTAAGTATGATTTCAACCCGACGCTGTCCGA 1416
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QY 1897 AAGCTTCAAGCAACATCACTACTACTAGTGTCTTGTCTTCTTCTTCTT 1956
DB 1179 AAGCTTCAAGCAACATCACTACTACTAGTGTCTTGTCTTCTTCTTCTT 1238
QY 1957 TTCTCTTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGT 2016
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DB 1299 CCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1358
QY 2077 ATCTGTCAAGCAACATCACTACTACTAGTGTCTTGTCTTGTCTTGTCT 2136
DB 1359 ATCTGTCAAGCAACATCACTACTACTAGTGTCTTGTCTTGTCTTGT 1418
QY 2137 CGGCAAGCAAGATGATGCTTGAAGACCTTCAAAAGATCTAGCTTGA 2196
DB 1419 CGGCAAGCAAGATGATGCTTGAAGACCTTCAAAAGATCTAGCTTGA 1478
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DB 1479 TGGAGCTTCTAGATGACATCTTCAAGTGTGGAAGATCTTCTTCTT 1538
QY 2257 ATGAGTGTGCTTACATGAGAGGCGCAAGAAAGTGTCTGAGAGCGAT 2316
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QY 2317 TCGCTTGTGCTTGTGTTTAAAGTGAAGTGTGTGTGGAAGCAATGAG 2376
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DB 1779 CAGTTGTGATGATGAGAGATTAATTAATTAATTAATTAATTAATTA 1838
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QY 2617 TGGATCTTATTAACCTTGAAGATTAAGAAAGAAAGAAAGAAAGAA 2666
DB 1899 TGGATCTTATTAACCTTGAAGATTAAGAAAGAAAGAAAGAAAGAA 1948

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RESULT 4
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 ID AAX23220 standard; DNA; 1650 BP.

AAX23220;
 11-JUN-1999 (first entry)

A. thaliana EL4 DNA.

EL4; very long chain fatty acid; VLCFA; beta-keto acyl synthase;
 plant; vegetable oil; lubricant; fuel; feedstock; plastic; cosmetic;
 pharmaceutical; edible oil; ss.

xx

OS Arabidopsis thaliana.
 XX W09854954-A1.
 XX 10-DEC-1998.
 XX 01-JUN-1998; 98MO-US11384.
 XX 03-JUN-1997; 97US-0868373.
 XX
 PA (CARGIL) CARGILL INC.
 PA (JAWORSKI) JAWORSKI J.G.
 PA (POST) POST-BEITENMILLER MA.
 PA (TODD) TODD J.
 XX
 PI Jaworski JG, Post-Beitenmiller MA, Todd J;
 DR WPI; 1999-070227/06.
 DR P-PSDB; AAW93430.
 XX
 PT New isolated beta-keto acyl synthase polynucleotides - used
 PT particularly for the production of transgenic plants having altered
 PT levels of very long chain fatty acids in tissues
 XX
 PS Claim 9; Fig 9; 76bp; English.
 XX
 CC This invention describes the isolation of beta-keto acyl synthase
 CC proteins from Arabidopsis thaliana. The products of the invention
 CC can be used for producing vegetable oils having elevated levels of
 CC very long chain fatty acids (VLCFA) for use as e.g. lubricants, fuels
 CC and as a feedstock for plastics, pharmaceuticals and cosmetics. The
 CC products can also be used for producing oils having reduced levels of
 CC VLCFAs for use as edible oils. This sequence encodes E14.
 CC
 XX
 SO Sequence 1650 BP; 429 A; 359 C; 407 G; 455 T; 0 other;
 Query Match 41.68; Score 1157.4; DB 20; Length 1650;
 Best Local Similarity 94.28; Pred. No. 1.4e-215;
 Matches 1243; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

Db 887 ACAAGTCAATGGTTATACCTAATGTTCTTAGAGATGGTTGTTCCGCCGTATAGCTCT 946
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 Db 1007 ATTAAGCTGCTGAGCACTTTGAGTTTCAATTCATTTTGGTAATTAATTCGTTTAC 1032
 Qy 1777 AATCTTGAACGACCTAGTAATTAATTTGTGCTTTTGAAGTGTGACAGGAAG 1836
 Db 1033 -----AGAGTGTGTACAGGAAG 1051
 Qy 1837 AAGATGAACAGANTTCAAGGGGTTGAAGATTAAGTACGACTTAATGAATTTGAGGTG 1896
 Db 1052 AAGATGAACAGANTTCAAGGGGTTGAAGATTAAGTACGACTTAATGAATTTGAGGTG 1111
 Qy 1897 AAGCTCTCAAGACAACATCACTACCTTAGGTCTCTGCTTCTACCTTCTCCGAGACG 1956
 Db 1112 AAGCTCTCAAGACAACATCACTACCTTAGGTCTCTGCTTCTACCTTCTCCGAGACG 1171
 Qy 1957 TTCTCTTCTTGTGCTTTGCTTGTGCTCGCCGACATTCCTCAGCTGTCGCAAAAGTCCACAA 2016
 Db 1172 TTCTCTTCTTGTGCTTTGCTTGTGCTCGCCGACATTCCTCAGCTGTCGCAAAAGTCCACAA 1231
 Qy 2017 CCACCTCTCTTCTACCTTCTCCGACCAACCAAGAAATGAATGAATGCTTCTCTCCG 2076
 Db 1232 CCACCTCTCTTCTACCTTCTCCGACCAACCAAGAAATGAATGAATGCTTCTCTCCG 1291
 Qy 2077 ATCTGTCCAAAGCCATATCCCGGACTCAAGCTCGCTTGCAGACATTTTGTCTCCAGC 2136
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 Db 1532 TCGCTTCCGTTTCTGCTTTAAGTGAACAGTGTGCTGGAAGCAATGAGAAAGTGA 1591
 Qy 2377 AGAAGCCAAACAGAAACAATCTTGGGTGAGTTCATCAACCGTTACCTGTGCTCTC 2435
 Db 1592 AGAAGCCAAACAGAAACAATCTTGGGTGAGTTCATCAACCGTTACCTGTGCTCTC 1650

RESULT 5
 AA090210
 ID AA090210 standard; cdna; 1810 BP.
 XX
 AC AA090210;
 XX
 DT 04-DEC-1995 (first entry)
 XX
 DE Brassica condensensing enzyme clone, CE15, from LEAR variety 212.
 XX
 KW Brassica; condensensing enzyme; CE15; ss.
 OS Brassica, LEAR variety 212.
 XX
 FH Key location/Qualifiers
 FT CDS 4..1650
 FT /*tag= a

XX MO9515387-A.
XX 08-JUN-1995.
XX 30-NOV-1994; 94WO-US13686.
XX 23-JUN-1994; 94US-0265047.
XX 30-NOV-1993; 93US-0160602.
XX (CALJ) CALGENE INC.
XX Lardizabal KD, Lassner MW, Metz JG;
XX WPI: 1995-215267/28.
XX P-PSDB; AAR77166.
XX Production of very long chain fatty acid(s) in plant(s) - to produce
XX drought and stress resistant transgenic plant(s)
XX
XX Claim 5; Figure 5; 149pp; English.
XX
XX Arabidopsis locus 39823 [sometimes called 398293] in Genbank
XX accession Z26005 is homologous to joboba beta-ketoadyl CoA
XX synthase DNA sequence. Two primers were synthesized - 090226
XX and 090227. 090226 corresp. to the peptide NITTLG, which is AAs
XX 389-394 of the joboba beta-ketoadyl-CoA synthase, and 090227
XX corresp. to the peptide SNCKRG, which is AAs 525-532 of the
XX joboba beta-ketoadyl-CoA synthase. These primers encode the
XX sense and antisense strands of the respective peptides. The primers
XX amplify an approx. 430 bp. DNA fragment from both the joboba
XX beta-ketoadyl-CoA synthase cDNA and the Arabidopsis 398293
XX sequence. Using the degenerate oligos, Arabidopsis green siliques,
XX HBAR, and LEAR RNA were subjected to RT-PCR. Prominent bands of the
XX expected size were amplified from all 3 RNAs. One clone obtd. from
XX the restion PCR reaction, and 2 clones from the 212/86 reaction,
XX which appear to be from two classes of cDNA clones, designated CE15
XX and CE20. The 212/86 CE15 clone encoded the entire CE protein
XX (090210/R77166). CE15 is expressed at high levels in leaves and at
XX a much lower level in developing seeds. The protein sequences of
XX CE15 and CE20 are almost identical. CE20 is highly expressed in
XX developing seeds and at very low levels in leaves.
XX
XX Sequence 1810 BP; 483 A; 408 C; 434 G; 485 T; 0 other;
XX
XX Query Match 33.3%; Score 927.2; DB 16; Length 1810;
XX Best Local Similarity 81.3%; Pred. No. 7.4e-171;
XX Matches 1188; Conservative 0; Mismatches 183; Indels 91; Gaps 6;
XX
QY 1114 TTTAGGTGCAAAAAGAGAGTTTCATAGACAGGAGAAATCAGGAGTTGACGAG 1173
DB 407 TTAAGGTGCAAAAAGAGAGTTTCATAGACAGGAGAAATCAGGAGTTGACGAG 466
QY 1174 AGACACTCGGTTTCAAGAGAGATCTTACAGGCTCAGGATAGGAGAGAGATAG 1233
DB 467 AGATCCCTCGGATTCAGAAAGAGATCTTACAGGCTCAGGATAGGAGATAGAG 526
QY 1234 TCCCAAGATCCATCTCTTCATCAGAAACATTAACAGATGAAGAGTGTGAAGAG 1293
DB 527 TCCCAAGATCAATCTCTTCGTCGAGAAACACACAGATGAAGAGTGTGAAGAG 586
QY 1294 CCTTCAGTGAATCTTTGAGACATAGAGAACTCTTCGAGAAAGACAGTGAACCTA 1353
DB 587 CTTGATGATGATATTTGGGCGACCTGACAGACCTCTTCGAGAAAGACAGTGAAC 646
QY 1354 AAGACGTGGTGTCTGTTGAGTAACTGATGATTTCAACCCGACACCGTCTGTCGG 1413
DB 647 AAGACGTGGTGTCTGTTGAGTAACTGATGATTTCAACCCGACACCGTCTGTCGG 706
QY 1414 CAATGATGATTAACCTTACAGATGAGAGGAACTACTAGTAAACCTTGAAGGA 1473
DB 707 CGATGATGATTAACCTTACAGATGAGAGGAACTACTAGTAAACCTTGAAGGA 766

QY 1474 TGGATGTGCGCTGGAATCATCTATGATCTTGGTCGAGACCTTTCAGTCAAC 1533
DB 767 TGGGTGCTGACGAGAGATCATCTATGATCTTGGTCGAGACCTTTCAGTCAAC 826
QY 1534 CTAAATGATGATCTGTTGTTGAGTACTGAGATGTTGGTAAATTTGATGAGGA 1593
DB 827 CGAATGATGATGATGTTGTTGAGTACTGAGATGTTGGTAAATTTGATGAGGA 886
QY 1594 GTGACAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1653
DB 887 GTGACAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 946
QY 1654 TCTTAACCGTGTGCTGATCTTTCGATGATGATGATGATGATGATGATGATGATG 1713
DB 947 TGTCTTAACCGTGTGCTGATCTTTCGATGATGATGATGATGATGATGATGATGATG 1006
QY 1714 CTCAATAGGCTGTGACGACCGTACGTTTCAATGATGATGATGATGATGATGATG 1773
DB 1007 CTCAATAGGCTGTGACGACCGTACGTTTCAATGATGATGATGATGATGATGATG 1035
QY 1774 TCAATCTCTGACCGACCTGATCAATATTTGTTGTTTGTAGAGTGTGACAGG 1833
DB 1036 -----AGGATGTGTACAGG 1051
QY 1834 AAGAAGATGAACAGAGATTCAGGGGTTGAGATAGTAACTAAATGAGATGAGAG 1893
DB 1052 AAGAAGATGAACAGAGATTCAGGGGTTGAGATAGTAACTAAATGAGATGAGAG 1111
QY 1894 GTGAAGCTCTCAAGACAAACATCACTAAGTCTCTTGTCTTACCTTTTCGAGG 1953
DB 1112 GTGAAGCTCTCAAGACAAACATCACTAAGTCTCTTGTCTTACCTTTTCGAGG 1171
QY 1954 AGCTTCTCTTCTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2013
DB 1172 AGCTTCTCTTCTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
QY 2014 CACACACTCTCTTCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2070
DB 1232 CACACT 1282
QY 2071 CTTCCGATCTGTCAGAGCATATATCCCGACTCAAGCTGCTGAGGATTTTGTCT 2130
DB 1283 CTTCCGATCTGTCAGAGCATATATCCCGACTCAAGCTGCTGAGGATTTTGTCT 1342
QY 2131 TCCACGGGGGCAAGAAATGATGCTTGAAGGCTTCAAAAATCTAGCTGATGAG 2190
DB 1343 TCCACGGGGGCAAGAAATGATGCTTGAAGGCTTCAAAAATCTAGCTGATGAG 1402
QY 2191 AGAATATGAGAGCTTCTAGATGATGATGATGATGATGATGATGATGATGATG 2250
DB 1403 AGAATATGAGAGCTTCTAGATGATGATGATGATGATGATGATGATGATGATG 1462
QY 2251 TCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2310
DB 1463 TCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1522
QY 2311 GGCAGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2370
DB 1523 GGCAGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1582
QY 2371 AGGTGAAGAGCCCAAGCAAGCAATCTTGGTGGATGATGATGATGATGATGATG 2430
DB 1583 AGGTGAAGAGCCCAAGCAAGCAATCTTGGTGGATGATGATGATGATGATGATG 1642
QY 2431 CTCTCTAATTAATCAATCTTCTAATTAATCAATCAATCAATCAATCAATCA 2490
DB 1643 CTCTCTAATTAATCAATCTTCTAATTAATCAATCAATCAATCAATCAATCA 1700
QY 2491 AAGATAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2548
DB 1701 TCTCTCTCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1760
QY 2549 TTATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2570

OY 2525 ACTGATCATCTCATCTAAGTCTGTTATAGAGATGATGCGTAGAGTCTGTTACGCT 2584
DB 140 ACTGATCATCTCATCTAAGTCTGTTATAGAGATGATGCGTAGAGTCTGTTACGCT 81
OY 2585 TCAACTGTTTATTTTGTGTTGTTCTCTAATGATCTTCAAACTTTGAGAGATTAA 2644
DB 80 TCAACTGTTTATTTTGTGTTGTTCTCTAATGATCTTCAAACTTTGAGAGATTAA 21
OY 2645 AGAAAAAACCTCTCTTAG 2664
DB 20 AGAAAAAACCTCTCTTAG 1

RESULT 7
AAC50606
ID AAC50606 standard; DNA; 1821 BP.
AC AAC50606;
XX
XX 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 65464.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0128845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
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PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145226.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.

PR	06-AUG-1999;	99US-0147302
PR	06-AUG-1999;	99US-0147416
PR	09-AUG-1999;	99US-0147493
PR	09-AUG-1999;	99US-0147935
PR	10-AUG-1999;	99US-0148171
PR	11-AUG-1999;	99US-0148319
PR	12-AUG-1999;	99US-0148341
PR	13-AUG-1999;	99US-0148555
PR	13-AUG-1999;	99US-0148684
PR	16-AUG-1999;	99US-0149368
PR	17-AUG-1999;	99US-01493175
PR	18-AUG-1999;	99US-0149416
PR	20-AUG-1999;	99US-0149722
PR	20-AUG-1999;	99US-0149723
PR	20-AUG-1999;	99US-0149902
PR	23-AUG-1999;	99US-0149930
PR	25-AUG-1999;	99US-0150566
PR	26-AUG-1999;	99US-0150884
PR	27-AUG-1999;	99US-0151065
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PR	27-AUG-1999;	99US-0151303
PR	31-AUG-1999;	99US-0151438
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PR	07-SEP-1999;	99US-0152363
PR	10-SEP-1999;	99US-0153070
PR	13-SEP-1999;	99US-0153758
PR	15-SEP-1999;	99US-0154018
PR	16-SEP-1999;	99US-0154039
PR	20-SEP-1999;	99US-0154772
PR	22-SEP-1999;	99US-0155133
PR	23-SEP-1999;	99US-0155486
PR	24-SEP-1999;	99US-0155659
PR	28-SEP-1999;	99US-0156458
PR	29-SEP-1999;	99US-0157511
PR	04-OCT-1999;	99US-0157696
PR	04-OCT-1999;	99US-0157752
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PR	13-OCT-1999;	99US-0159294
PR	13-OCT-1999;	99US-0159255
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PR	14-OCT-1999;	99US-0159330
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PR	25-OCT-1999;	99US-0161404
PR	25-OCT-1999;	99US-0161405
PR	25-OCT-1999;	99US-0161359
PR	26-OCT-1999;	99US-0161360
PR	26-OCT-1999;	99US-0161361
PR	28-OCT-1999;	99US-0161920
PR	28-OCT-1999;	99US-0161993
PR	28-OCT-1999;	99US-0162142

Query Match	10.7%	Score 298.4;	DB 21;	Length 1821,
Best Local Similarity	55.7%;	Pred. No. 1.1e-48;		

Matches	737: Conservative	0: Mismatches	446: Indels	141: Gaps
QY	1128	GAAGAGTTTCATAGAACTTAGCGAGAAAATATCAGGGAGAGTTGAGACAGAGAGACACTCGGTTC	1187	
Db	521	GAACATTCATGACAGATCTCAACGCTGTAGGATCTTCACAGAAAGACAACCTAGCTTTC	580	
QY	1188	AAGAAGAGATCTTACAGAGCTCAGGCATATGGCGACGAGACATATAGTCCCAAGATCATC	1247	
Db	581	CAACAAAAGATCCTCGAAGATCCGGCTTAGGTCAAGAAAACCTTACTTCCCTAAGCTCTT	640	
QY	1248	TCCTCATCAGAAAACATATACAGATGAAGAAAGGTCTGGAAGAGCCCTACATGATC	1307	
Db	641	CTTCGTGTCTCTCTATATCTTGTATGAAAGAGCGAAGAAAGAGCGAAGAAACCTATTATG	700	
QY	1308	TTTGGAGCACTAGACGAACTCTTCGAGAGACAGCTGTAAACCTAAAGACGTGGTGC	1367	
Db	701	TTGGAGCTATTGACCGGGTCTTGAGAAAGACCGGGTGAACCTTAAGATATTGGAATC	760	
QY	1368	CTTGTGTTACTGTAGCATTTTCAACCCGACACCGTCGTTGCGCAATGGTGTAAAC	1427	
Db	761	CTTGTGTGTAATGTAGCTGTGTTATATCCAAACCGTCACTTTCGTATGATGTGAAT	820	
QY	1428	CATTACAAAGTGGAGAGGAAACATACTATTACAAACCTTGGAGGATGGATGTGGCT	1487	
Db	821	AAATATATAGCTTAGAGCAACATTTTGACCTTAAATCTTGGATGGAATGGAGATGAGTCT	880	
QY	1488	GGAATCATAGCTATTGATCTGCTGTCGACATGCTTACAGCTTAACCTTAATAGTATGCT	1547	
Db	881	GGCCTTATCTCATGTATCTCGTTAAACAGATGCTTACAGTGCACAAACCTATACGCA	940	
QY	1548	GTTGTTGTAGTACTAGATGGTGGGTATTAATGGTACGTGGAGATGGACAACTCAATG	1607	
Db	941	CTAGTGGTAGGACACAGAGAACATTAACCCTAACCTGTACTTATAGCCAAAGACGATCAATG	1000	
QY	1608	GTAATACCTAATATGTTTCTTTAGAGAGGGGTGTCTGCGGTATAGCTCTTAAACCTGCT	1667	
Db	1001	CTTCTATCTTAAGTATCTTCGTAATGGCGGAGCGCGGGATCACTTCTTCGAAACCGCTCC	1060	
QY	1668	CGTAGCTTTCGCAATGCTAATGACGCTCGACGACATGTCGGAATCATTAAGAGCT	1727	
Db	1061	TCGTATCGAGCGCTTCAAAATATACGCTCATCCATACCGTCCGTAACCCAAAGAGACT	1120	
QY	1728	GACGACCGTAGCTCAGCTTTCATTCATTTGGTATTAATCGTTTAACTCTCTTGAC	1787	
Db	1121	GATGAC-----	1126	
QY	1788	CGACCTAGTAACATAATTTTGTGTGGTTTTATAGAGTGTGTACCGAAGAAAGATGAACAA	1847	
Db	1127	-----AAGCATTTTGGCTGTGTTTACCAACGAGAAAGCAACAACGCAAGAAAGAACCC	1177	
QY	1848	GGATTCAAAGGGGTTAAAGATATAGTAGAGACTTAATGSAAGTTGGAGGTGAAGCTCTAAG	1907	
Db	1178	GGCAAAATCGAGGTGTCCCTCTTAAAAACCTAATGGGATAGGTGGAGAAAGCTCTAAG	1237	
QY	1908	ACAAACATCACTACCTTAGGTCTCTTTCCTTACCTTTCCTCGACAGTCTCTTCTT	1967	
Db	1238	ACAAACATCACTACCTCGAGCACTACTTCTACCAATGTCCGAACAACCTTCTCTTTC	1297	
QY	1968	GCTGCTTGTCTCCGGCAACATCTCACCTCTGCGCAAAACGTCACACACACTTCTTC	2027	
Db	1298	GGGACTCTTGTGGCCGAAAGTCTTCAAACTCAAGAAA-----	1337	
QY	2028	TCTACTTCGCGACGCAAAAACCAATGGAATCAAGTCTTCTCTTCGATCTGTCCAAG	2087	
Db	1338	-----TAAAG	1342	
QY	2088	CCATACATCCGGAATACAGCTCGCTCGAGCATTTTGTCTCCACGGCGAAGCAAA	2147	
Db	1343	CCTTACATTCCTGATTTCAACGCTTTCGAGCATTTCTGTATCCACGCGGAGGTAGA	1402	
QY	2148	GTAAGCTTGAAGACTTCAAAAGATCTAGGCTTGTAGTAGAAGATATGAGGCTGT	2207	
Db	1403	GCCGCTGCTCGAGATTTGAGAAACCTTGGAATTTATCCGATATGGCATATGAGGAGCATG	1462	

Db 1199 AGCATATACATCCAGATTTCAGATTGGCAGCGAGCACTTCTGCATCCATGACGAGAGCA 1258
 QY 2146 AAGTAGTCTTGAAGAGCTTCAAAAGAAATCTAGGCTTGAGTGAAGAAATATGAGGCTT 2205
 Db 1259 AAGCAGTGTGATGATGCTCCGAGACGAACCTTGAAGTTCAGCCATGCGCACTTGAACCTT 1318
 QY 2206 CTAGAGTACACTTCAAGGTTTGGAAACACTTCTAGCAGTGGAAATCTGGATGAGTTGG 2265
 Db 1319 CGAGATGACACTGTATGAGTTTGGGAACACATCATGAGTGCATATATGTCAGAGTTGG 1378
 QY 2266 CTATATGAGAGCCCAAGAAATGTTCCGTAAGGCGGATGAGGTTTGGCAGATCGCTTTCG 2325
 Db 1379 CATACGCTGAACCAAAAGGAGAGATCCGTAAGGTCATCGAACTTGGATGATGATTTGG 1438
 QY 2326 GTTCTGTTTATGATTAACAGTGTGATGAGGCAATGAGAGTGAAGAGAGCCAA 2385
 Db 1439 GTTCAAGTTTCAAGTGAACATGTTGTGTGAGAGGCTTGTGAGAGTGTCAATCCGCGCTA 1498
 QY 2386 CCAGAGCAATCTTGGGTGATGATCAGTACACCGTTACCCCTGCTCTTAATTTATCA 2445
 Db 1499 GAGAGAGAAATCTTGATGATGAATAATTGAGAATTTCCCTGTCATGTGCTTAATCG 1558
 QY 2446 TTCTCTTAAT 2457
 Db 1559 CACCTATCGCTT 1570

RESULT 9

AA090208 standard; cDNA: 1783 BP.

AA090208;

04-DEC-1995 (first entry)

Jojoba fatty acyl-CoA cytoplasmic protein cDNA in pCGN7614.

Very long chain fatty acid; fatty acyl-CoA; ss.

Jojoba.

Key Location/Qualifiers

CDS 10..1575

/*tag= a

M09515387-A.

08-JUN-1995.

30-NOV-1994; 94WO-US13686.

23-JUN-1994; 94US-0265047.

30-NOV-1993; 93US-0160602.

(CALJ) CALGENE INC.

Lardizabal KD, Lassner MM, Metz JG;

MPI: 1995-215267/28.

P-PSDB: AAR77165.

Production of very long chain fatty acid(s) in plant(s) - to produce

drought and stress resistant transgenic plant(s)

Example: Fig 3; 149pp; English.

RNA is isolated from Jojoba embryos and used to construct a cDNA

library. Synthetic oligos are synthesised which corresp. to the

AA sequences of selected peptide fragments and segments of DNA

are produced. The DNA fragments obtd. by PCR are labeled and used

as a probe to screen clones from the cDNA libraries. An approx.

1500 nt. Jojoba cDNA clone is obtd. in this manner. Comparison

to the peptide fragments in AAR77175-R77182 reveals the presence of

CC each of these peptides in the translated sequence, with the
 CC exception of 501129. The mRNA is approx. 2kb. Preliminary DNA
 CC sequence of a Jojoba gene is presented in AA090107/R77164. Further
 CC DNA sequence analysis of additional clones indicates that there are
 CC at least 2 classes of cDNAs encoding this Jojoba protein. The
 CC plasmid contg. the entire coding region in pCGN1703 is constructed
 CC to contain a SalI site approx. 8 nts 5' to the ATG start codon and
 CC is designated pCGN7614. The complete DNA sequence of pCGN7614 is
 CC given in AA090208/R77165. The major difference between the two
 CC classes of cDNAs is the presence (AA090207) or absence (AA090208) of
 CC the 6 nt coding sequence for AAs 23 and 24 of AAR77164.

Sequence 1783 BP; 450 A; 446 C; 432 G; 455 T; 0 other;

Query Match 10.7%; Score 296.8; DB 16; Length 1783;

Best Local Similarity 55.2%; Pred. No. 2.3e-48; Matches 735; Conservative 0; Mismatches 447; Indels 150; Gaps 2;

QY 1126 AAGAGAGTTCATATAGAACTAGCAGAAATACAGGAAGTTGACGAGAGACATCGGTT 1185
 Db 389 ACGAGATGTTATGACCGGACCTCCCGGCGGCGTTTCTTAAGAGAAATATGAGT 448
 QY 1186 TCAAGAGAGGATCTTACAGGCTCAGGATAGGCGAGCAGCATACGTCCTCAAGATCCA 1245
 Db 449 TTCAGAGGAAGATCTTGGAGAGGCGGATATGGCGGGAACCTTACGTCCTCGAATCG 508
 QY 1246 TCTCTTCATCAGAAAACATATACAGATGAAAGAGTGTGTAAGAGCCCTCTACAGTGA 1305
 Db 509 TCACATAGAGTGGCGCCGAGCCGAGCATAGCAGCAGCCAGGCGGAGAGAGATGA 568
 QY 1306 TCTTGGAGCACTATGACAACTCTTCGAGAGACAGCATGTAAACCTTAAGACGTTGGTG 1365
 Db 569 TGTACGGGGCGATTCAGCAGGATGTGGAGAAACGCGGGGTGAAGCCGAAGATAGGAA 628
 QY 1366 TCTTGGTGTATAGTATGATTTCAACCCGACACCGCTGTGTCGGAATGATGA 1425
 Db 629 TACTGGTGTGACACCTGATTTAACCAACCGCTGTGTCATCATGATGATGA 688
 QY 1426 ACCATTACAGATGAGAGGAGCAATACCTAGTAAACCTTGGAGGATGGATGTTGCG 1485
 Db 689 ACCATTACAGCTTAGGGGTAATATATAGCTATATATCTTGGTGGATGGTTGACAGT 748
 QY 1486 CTGGAATCATATGCTATGATCTGCTCGTACATGCTTACGTCATACCTAATAGTATG 1545
 Db 749 CTGGGCTCATTTCCATGATCTTGGCAAGAGACCTCTAGAGGTTAACCTTACATATAG 808
 QY 1546 CTGTGTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1605
 Db 809 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 868
 QY 1606 TGTATATACCTAATGTTCTTTAGGATGGTGTGCTGCTGCTTACCTTAAACCTGTC 1665
 Db 869 TGTATATACCAAGTCCATTTGCGATGGTGGGCGCTCATATCTTCAAAACCGGT 928
 QY 1666 GTCTGATCTTGGCCATGCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1725
 Db 929 GCGGTGATGCTGCGGATCCAAAGTACCAACTCTTACACAGATAGCAACCCCAAGGGGG 988
 QY 1726 CTGACGACCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1785
 Db 989 CTGACGAC-----AGTCTATATGATGATGATGATGATGATGATGATGATGATGATGAT 996
 QY 1786 ACCGACCTAGTAACTAATTTGTGTGTTTATGAGAGTGTACACAGAGAAAGATGAAC 1845
 Db 997 -----AGTCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1033
 QY 1846 AAGATTCAAGGGGTTGAAGATATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAG 1905
 Db 1034 ATTAACAGGATAGTGTGCTTATCAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1093
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 Db 1094 AGGCCAACATCAACGACCTTGTGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1153

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 QY 1187 CAGAAGAGATCTTACAGCCTCAGCAGATAGCGAGACATACCTCCAGATCCAT 1246
 DB 579 CAACAAAGATCCTCAAAAGATCCGCTAGTCAAGAACTTACTTCCCTGAACCTC 638
 QY 1247 CTCCTATGAGAAACATTAACACATGAAGAGTCTGAAGAACCTTACATGATCAT 1306
 DB 639 TCTTCGTTCCTCCATATCCTTGTATGAGAGAGAGAGAGAGAGACATTTAT 698
 QY 1307 CTTTGAGCAGTATGACGACCTCTTCGAGAGACAGCTTAACCTTAAGACCTTGGT 1366
 DB 699 GTTCGAGCTATTTAGCCGCTCTTTCAGAGACCGGTGCAACCTTAAGATTTGGAT 758
 QY 1367 CCTGTGTGTTAACTGATGATTTTCAACCCGACACCGTGTCTCCGCAATGGTGAATA 1426
 DB 759 CCTTGTGTGTAATTTAGCTTGTATTCACACACCGTCACTTGTGTATGATTTGAA 818
 QY 1427 CCATTCAAGATGAGAGGAGAACATTAATTGTTTCAACCTTGGAGGATGGATGTTCCG 1486
 DB 819 TAAGTATTAAGCTTAGAGGCAACATTTTGAATATAATCTTGTGGAATGATGATGC 878
 QY 1487 TGAATCATGATGATGATCTCTGTCGACATGCTTCAAGCTTAACCTTAATGATATGC 1546
 DB 879 TGCCCTTATCTCATTTGATCTCGCTTAACAGATGCTTCAGGTGACCAACCACTCATAC 938
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 DB 939 ACTAGTGTGAGACAGACAGACATTAACCTTAACCTGATCTTATAGGACAGACGATCAAT 998

Db 816 TGTTCCTAGTGAACATTACTCAGATTGATTTGTTGGTAACAGAAATCATGTTGAT 875
Oy 1613 ACCTAATTGTTCTTAGATGGTGTCTCCGTTATGCTCTTAACCGTGTGTGA 1672
Db 876 ACCGAAGTCTGTTGTTGAGTGGTGGCTCGGTTTTCCTATCGAACAAGTCGAGGA 935
Oy 1673 CTTTCGCCATGCAATGACCGTCTGAGCACAATGTCGAAACATTAAGCGTCTGACGA 1732
Db 936 CAAGAGACGGTCTAAGTAAAGGCTTACATGTAGTCAGACACTCACCCTGAGCAGATGA 995
Oy 1733 CCGTACCTCAGGTTTCATTCATTTGGTAATTCGTTTACAAATCTCTTGACCGACC 1792
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Oy 1793 TAGTACTAATTTTGTGTGTTTGTAGAGTGTCTACCGAAGAAAGATGACAGGATT 1852
Db 996 -----TAAAGCTTCCGTTGTGTTTATCAAGACAGAGATGATCAGAGGAG 1040
Oy 1853 CAAGGGTGAAGATAGTAAAGTAAAGTGAAGTGGAGTGAAGCTCTCAAGACAA 1912
Db 1041 AACCGGGGTTTGTCTCGAAGATCTAATGCGATTGCAAGGGAACTCTCAAAACCA 1100
Oy 1913 CATCACTACCTTAGTCTCTTGTCTCTACCTTCTCCGAGCAGCTCTCTTCTTGTGTC 1972
Db 1101 TATCACTAATTTGGTCTCTCTGTCTACCGATAAGTGAAGCAGATCTCTCTT----- 1155
Oy 1973 TTGTGCTCCGCGACATCTCACCTGTCGCAAAAGTCCACAAACCTCTCTCTAC 2032
Db 1156 ----- 1155
Oy 2033 TTCGCGCACGCAAAACCAATGAAATCAAGTCTCTCTCTGATCTGTCAAGCCATA 2092
Db 1156 -----ATGACTCTAGTTGTGAAAGACTCTTTAACGTAAGTGAACCGTA 1202
Oy 2093 CATCCGGACTACAACTGCTTCGAGCATTTTCTCTCCAGCGCAAGCAAGTAGT 2152
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Db 1263 GATCGATGATTAAGAAAGATCTGACGTTTCACAGTCAATGAGCTTCGAGAT 1322
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Oy 2273 GGAGGCCAAGAAAGTGTCTAGAGCGATAGGTTTGGCAGATCGCTTCGTTCTGG 2332
Db 1383 TGAAGCGAAGGAGATGCGAAGAGTAAATCTGTTTGGCAAAATCGCGTTGGAAGTGG 1442
Oy 2333 TTTTAAAGTGAACATGCTGTGTGAAGGCAATGAGGAAGTGAAGCAACCGAGGA 2392
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Oy 2393 CAATCTGCTGGTGCATGATCAACCGTTACCTGTGCTCT 2434
Db 1500 CAGTCTTGGGAAGATTGTATGACAAGTATCCGTTACTTT 1541

RESULT 13

AAC42778
ID AAC42778 standard; DNA; 1464 BP.

AAC42778;

17-OCT-2000 (first entry)

Arabidopsis thaliana DNA fragment SEQ ID NO: 36814.

Hybridisation assay; genetic mapping; gene expression control;

protein identification; signal transduction pathway;
metabolic pathway; promoter; termination sequence; ss.KW
XX

OS Arabidopsis thaliana.
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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DB 335 ATTTGAGGAAACCTCTCTGTGATTCAGAGAGATCTTGATTCGCTCGGTG 394
QY 1222 ACGAGACATAGCTCCAGATCTCTTCATCAGAAACATACAGATGAAGAAG 1281
DB 395 AAGACACTTATTACCGGATCTATTCACCTATCCCGGCTCTACTATAGGCTGAG 454
QY 1282 GTCTGGAAGAACCTCTACATGATCTTTGGACACTAGACAGACATCTTCGAGAAGAC 1341
DB 455 CCGGTGAAGAACCGGAGGAGTAATCTCGGTGACCTGACATCTTTTCGAGATACAA 514
QY 1342 GTGTAAACCTTAAGACGTGGTCTCTTGCTGTGCTTAACCTGTAGCAATTTCAACCCGAC 1401
DB 515 AATCAATCTTAGGAGATGGTGTCTGTGTAATGTAGTTGTTAAACCTTACGC 574
QY 1402 CGTCGTTCGCAATGGATGAATACCAATTAACAGATGAGAGGAACATTAATTAACA 1461
DB 575 CTTCCTTTATCCGCCATGATGTTAACAAGTATAGACTTAAGAGACATTAAGACCTTTA 634
QY 1462 ACCTTGAGGAGATGGATGCTCGCTGGAATCATAGTATGATCTCTGCTGACATGC 1521
DB 635 ACCTTGAGGAGATGGATGCTGCTGATGATGCGGTAGATAGTACTAGTATGATGT 694
QY 1522 TTCAGTCAACCTTAATAGTTATGCTGTGTGTGTAGTACAGTATGATGCTGATATTT 1581

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Db 695 TACAATGCAATGAGAACACTTTGCTTGTGTAGTACGTGAGAACATCACTCAGAAAT 754
Oy 1582 GGTACGTGGGAAGTACAGCAATGATGTTATACCTAATTTGTTTGTAGAGGTGTT 1641
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Db 755 GGTATTTTGTGTAACAGAAAGCAATGTGATCCCTAATTTGCTTTAAGTTGGTGT 814
Oy 1642 CTGGCGTTATGCTCTGATACCGTGTGCTGCTTTCGCACTTTCAGTACGCTCGAGC 1701
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Db 815 CCGCGTTTCTGCTTTCGACCAAGCCCTTGGATCGAAAGATCAAGTATTAAGCTTGTTC 874
Oy 1702 ACATTTGCGAATCATAGGCTGCTGACGACCGTACGCTTTCAGTTCATTTATTTGGT 1761
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Db 875 ATAGGTCGAGACATCAATAAGATCTGATGAGAACGACATTCATTT----- 919
Oy 1762 ATTAATTTGCTTTACAACTCTTGACCGACCTAGTAATTAATTTTGTGTTTATGGA 1821
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Db 920 ----- 919
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Db 920 GTGTGTATACAGAACAGATGATGTTGTAACACCGAGTTCTTGTGTAAAGATCTTA 979
Oy 1882 TGGAAATTGAGAGTGAAGCTCTCAAGACAAACATCACTAAGTTCCTCTTGTCTTAC 1941
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Db 980 TGGTATAGCTGAGAGAGCTTAAAGACGATATACCTTTTGGGCTCTGTTCTTTC 1039
Oy 1942 CTTCCTCGAGAGCTTCTCTTCTTGTGCTTGTGCTCGCGCAACATTTCTACCTGCTG 2001
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Db 1040 CTATAGGAGAGAGATTTGTTCTTGTTCGACCTTTGT----- 1076
Oy 2002 CCAAAAGCTCACAAACACTTCTCTCTACTTCCGCCACCGCAAAACCAATGGAATCA 2061
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Db 1085 GATTTGTCAATGACAAAGAAAGAACCCCTTACATCCGATTCGAGCTTGTCTTATGATC 1144
Oy 2122 ATTTTGTCTTCACGCGGAGCAACAAAGTATGCTTGAAGAGCTTCAAAAGATCTTAGC 2181
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Db 1145 ATTTCTGATTTCCGCGGAGGTAGAGCCGATTTGATGAGTGAAGAGATTTTAAAGC 1204
Oy 2182 TGAAGTGAAGATATGAGAGCTCTAGAGTACACTTACAGGTTTGAACACTTCTA 2241
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Oy 2242 GCAATGGAATCTGTATGATGCTTACATGAGAGCCCAAGAAAGTCTCTAGAGCGC 2301
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Db 1265 CTAGCTCTATATGATGATGATGCTTACACGAAAGCTTAAAGAAATGAGAAAGAA 1324
Oy 2302 ATAGGTTTGGAGATCGCTTTCGGTTCGTTTAAAGTGAACAGTGTGCTGGAAG 2361
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Db 1325 ACAGATTTGGAGATTTGTTTGGTAGCGGTTTAAAGTAAACGCGGTTTGGGTGG 1384
Oy 2362 CAATGAGAAAGTGAAGAACCAACAGAGCAATCTTGGGTGATGATCAACCTT 2421
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Db 1385 CTCTTCGCAATGT---CGAGCCCTCGGTTAAACAATCCTTGGGAACTTGCATCAATGAT 1441
Oy 2422 ACCCTGCTCTCTTAATTT 2441
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Db 1442 ATCCGCTTAAAGATGATCTT 1461
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RESULT 14

AAf62693 standard; DNA; 2509 BP.

AAf62693:

08-MAY-2001 (first entry)

Arabidopsis KCS2 genomic DNA.

XX

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KW Long chain fatty acid condensing enzyme; KCS2;
KM beta-ketoacyl-coenzyme A synthase 2; cosuppression; antisense;
XX screening; ds.
XX
XX Arabidopsis sp.
XX
XX W0200107586-A2.
XX
XX 21-JUL-2000; 2000WO-CA00860.
XX
XX 01-FEB-2001.
XX
XX 22-JUL-1999; 99US-0145013.
XX
XX (UYBR-) UNITV BRITISH COLUMBIA.
XX
XX Kunst L, Clemens S;
XX
XX WPI: 2001-168548/17.
XX
XX Novel nucleic acid sequence encoding plant long chain fatty acid (LCFA)
XX condensing enzyme (fatty acid elongase) useful for producing transgenic
XX plants having altered fatty acid content in the tissues
XX
XX Example 1; Fig 1; 32pp; English.
XX
XX The present invention relates to a plant long chain fatty acid
XX condensing enzyme, KCS2 (beta-ketoacyl-coenzyme A synthase 2).
XX The invention is useful in cosuppression or antisense inhibition,
XX as a plant breeding tool, as molecular markers to aid in plant
XX breeding programs and in screening
XX
XX Sequence 2509 BP; 748 A; 478 C; 497 G; 786 T; 0 other;
XX
Query Match 10.1%; Score 281.6; DB 22; Length 2509;
Best Local Similarity 55.7%; Pred. No. 2.2e-45;
Matches 713; Conservative 0; Mismatches 414; Indels 153; Gaps 3;
Oy 1162 ACTTGACGCAAGAGACACCTCGGTTTCAAGAAAGATCTTACAGGCTCAGCATRGGC 1221
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Db 1380 ATTTGACGCAAACTTCTTGAAGTCCAGAGAAATCTTGATTCGCTGTGCTGCGTG 1439
Oy 1222 ACGAGCATACGTCCCAACATCTCTCATCAGAAAAACATCAACAGATGAAGAAG 1281
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Db 1440 AAGAGCTTATTTACCGGATTTCTATTCATCTATCCCTCGGCTCTACTATGCTGCG 1499
Oy 1282 GTCTGTAAGAGACCTCTCTACAGTATCTTGAAGCACTAGACGAATCTTGAGAGACAC 1341
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Db 1500 CCGGTGAAGAAAGCGAGAGATTAATCTCGGCACTCGACAATCTTTCGAGAAATACAA 1559
Oy 1342 GTGTAAACCTTAAGACGTTGTGCTCTGTGTTAACTGTAGCATTTTCAACCCGACAC 1401
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Db 1560 AATTCATCTCCTAGGAGATTTGCTTGTGTTGATTTGATTTGTTTAAACCTTACGC 1619
Oy 1402 CGTCTGTTGCCCAATGATGATAAACATTACAAAGATGAGAGGAACATTAAGTTACA 1461
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Db 1620 CTCTTTATCCCGCATGATTTGTTAACAAATTAAGCTTAGAGAAACATTAAGAGCTTAA 1679
Oy 1462 ACCTTGAGAGATGGAGATTCGGCTGGAATCATAGCTTAATGATCTTGTCTGACATGC 1521
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Db 1680 ACTTGGAGGAATGGATGTAGCTGTGTTATCCGAGTAGATCTAGTAGATGATATGT 1739
Oy 1522 TTCACTTAACCTTAATTAATTAATGCTGTGTGTGAGTACTAGATGATGTTGGTATAAT 1581
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Db 1740 TACAATTCATAGGAACACTTTTGTCTTGTGTGATGACTGAGAACATCACTCAGAAAT 1799
Oy 1582 GGTACGTGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1641
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Db 1800 GGTATTTTGTGTAACAGAAAGCAATGATCCCTAATTTGCTTTTAAAGTTGGTGT 1859
Oy 1642 CTGCGTTATGCTCTTAACCGTGTGCTGATCTTTCGCAATGATGATGATGATGATGATGAT 1701
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Db 1860 CCGCGTTCTGCTTTCGACAGAGCTTTGATCGAAAGATCAAGATCAAGTATTAAGCTTGTTC 1919
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PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 19-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
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PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
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PR 23-JUL-1999; 99US-0145145.
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PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
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PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 23-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.

PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
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PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 23-OCT-1999; 99US-0161040.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 10.0%; Score 278; DB 21; Length 1587;
Best Local Similarity 54.9%; Pred. No. 1e-44;
Matches 700; Conservative 0; Mismatches 430; Indels 144; Gaps 2;

QY 1122 ACAAGAGAGATTTCTAGACTAGCGAGAAATCGAGGAGGAGGAGACATC 1181
DB 364 ACACGAGAAACGTTTACGTGACCGGCTTCACCGCTGCTGATCTTCCACAGAACAACTTC 423
QY 1182 GATTTCAGAGAGATCTTCAAGCCTCAGCATAGCGCAGCAGACATACGTCGCAAGA 1241
DB 424 GCTTCCACAAAGATTCCTCGAAGCTTCGCGCTTGAGACAAAGACTTCTCCGGAG 483
QY 1242 TCCATCTCTTCATCAGAAACATACACAGATGAAAGAGCTGTCAGAGAGCTCTACA 1301
DB 484 GCTCTCTTACGTGCTCCGCTTAATCTTGTATGCTGAAACAGAAAGACCGGAGACG 543
QY 1302 GTGATCTTGGAGCAGTACGAGCAACTTCGAGAAAGACAGTAAACCTTAAGAGCTT 1361
DB 544 GTTATGTTTGGAGCTATAGCGCAGTCTTGAGAAACCGGAGTGAATCTTAAGATATT 603
QY 1362 GGTGCTCTTGCTGTTAAGTCTATACATTTTCACCCGACACCGTGTGTCGCAATGNG 1421
DB 604 GGATACCTTGTCTGATTTGCTATGCTTTAAATCCGACGCTTCGTTATGCGTATGATC 663
QY 1422 ATAAACCATTAAGATGAGAGGAGAAACATTAAGTTTACACCTTGAGAGGATGGATGT 1481
DB 664 GTGAATAAATATATAGCTCAGGAGAAACGTTTGTAGCTATTAACCTTGATGAATGGGTTGT 723
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QY 1542 TATGCTGTTGTTGAGTACTGATGATGATGTTGGTATTAATGTTACGTCGGAAGTGAAC 1601
DB 784 TATGCACTGATGATGAGCAGACAGAAACATTAACCTTAACCTTAACCTTAACCTTAACCTTA 843

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1	1157.4	41.6	1650	4	US-08-868-373-7	Sequence 7, Appl
2	296.8	10.7	1783	1	US-08-066-299-11	Sequence 11, Appl
3	296.8	10.7	1783	1	US-08-265-047-3	Sequence 3, Appl
4	283.2	10.2	1548	4	US-08-868-373-13	Sequence 13, Appl
5	275.4	9.9	1733	1	US-08-265-299-10	Sequence 10, Appl
6	275.4	9.9	1733	1	US-08-265-047-2	Sequence 2, Appl
7	275.4	9.9	1733	4	US-08-926-522-21	Sequence 21, Appl
8	269	9.7	1560	4	US-08-868-373-9	Sequence 1, Appl
9	268.4	9.6	1611	4	US-08-868-373-9	Sequence 9, Appl
10	249	9.0	1502	4	US-08-868-373-11	Sequence 11, Appl
11	247.4	8.9	1481	4	US-09-058-847A-3	Sequence 1, Appl
12	247.4	8.9	1807	4	US-09-058-847A-2	Sequence 2, Appl
13	247.4	8.9	3722	4	US-09-058-847A-1	Sequence 1, Appl
14	210	7.5	1641	4	US-08-868-998-1	Sequence 1, Appl
15	210	7.5	1641	4	US-09-362-633-5	Sequence 1, Appl
16	206.2	7.4	1512	4	US-08-868-373-5	Sequence 5, Appl
17	189.2	6.8	1479	4	US-08-868-373-3	Sequence 3, Appl
18	67.6	2.4	6124	4	US-08-213-419B-3	Sequence 3, Appl
19	59	2.1	383	3	US-08-868-998-3	Sequence 3, Appl
20	59	2.1	383	4	US-09-362-633-3	Sequence 3, Appl
21	58.2	2.1	6265	4	US-09-129-112-3	Sequence 3, Appl
22	57	2.0	5852	1	US-07-867-106-2	Sequence 2, Appl
23	56.8	2.0	20674	4	US-09-161-638-651	Sequence 651, Appl
24	55	2.0	998	4	US-09-422-400B-5	Sequence 5, Appl
25	53.4	1.9	665	2	US-08-863-795A-36	Sequence 36, Appl
26	53.2	1.9	19124	2	US-08-487-826B-13	Sequence 13, Appl
27	53	1.9	665	2	US-08-863-795A-36	Sequence 36, Appl

28	53	1.9	2237	3	US-09-157-077-1	Sequence 12, Appl1
29	52.8	1.9	2216	1	US-08-046-583-12	Sequence 1, Appl1
30	52.8	1.9	2216	1	US-08-384-5566-3	Sequence 3, Appl1
31	52.8	1.9	2216	2	US-08-331-3555-24	Sequence 24, Appl1
32	52.8	1.9	2216	5	PCT-US94-12364-24	Sequence 24, Appl1
33	52.8	1.9	2216	5	PCT-US95-07753-3	Sequence 7, Appl1
34	52.8	1.9	2238	3	US-09-157-077-7	Sequence 7, Appl1
35	52.2	1.9	615	4	US-08-598-416-186	Sequence 186, Appl1
36	52.2	1.9	6124	4	US-08-213-4196-3	Sequence 3, Appl1
37	51.2	1.8	782	4	US-09-007-119-15	Sequence 15, Appl1
38	50.8	1.8	3701	4	US-08-945-558-10	Sequence 10, Appl1
39	50.8	1.8	3701	4	US-08-950-571-10	Sequence 10, Appl1
40	50.8	1.8	3701	4	US-08-723-142-10	Sequence 10, Appl1
41	50.8	1.8	3701	4	US-09-528-784-10	Sequence 10, Appl1
42	50.2	1.8	7218	1	US-08-332-663-14	Sequence 14, Appl1
43	50	1.8	7311	1	US-08-651-405-2	Sequence 2, Appl1
44	49.8	1.8	660	1	US-07-991-967-32	Sequence 32, Appl1
45	49.8	1.8	660	1	US-08-107-353A-32	Sequence 32, Appl1

ALIGNMENTS

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US-08-868-373-7
RESULT 1
:
: Sequence 7, Application US/08868373
: Patent No. 6307128
: GENERAL INFORMATION:
: APPLICANT: Jaworski, Jan G.
: APPLICANT: Post-Belttemiller, Martha A.
: APPLICANT: Todd, James
: TITLE OF INVENTION: PTXY ACID ELONGASES
: FILE REFERENCE: 07148/064001
: CURRENT APPLICATION NUMBER: US/08/868,373
: CURRENT FILING DATE: 1997-06-03
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 7
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: LENGTH: 1650
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: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-08-868-373-7

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Query Match	41.6%;	Score 1157.4;	DB 4;	Length 1650;
Best Local Similarity	94.2%;	Pred. No. 6.9e-246;		
Matches 1243;	Conservative	0;	Mismatches 1;	Indels 75; Gaps 1;

Qy	1117	AGGAGCAAAAAGAAAGAGTTTCATGACCTACGCGAGAAAATCAGGAGAACTTCACGCAAGAGA	1176
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Qy	1177	CACTCGGTTTCAGAGAGAGCATCTTTCAGAGCCTCAGGCATAGGCGACGAGACATACGTTCC	1236
Db	467	CACTCGGTTTCAGAGAGAGCATCTTTCAGAGCCTCAGGCATAGGCGACGAGACATACGTTCC	526
Qy	1237	CAAGATCCATCTCTTCATCAGAAAATATAACAACGATGAAAGAGTGCTGTAAGAAAGCTT	1296
Db	527	CAAGATCCATCTCTTCATCAGAAAATATAACAACGATGAAAGAGTGCTGTAAGAAAGCTT	586
Qy	1297	CTACAGTGATCTTTGGAGACACTAGACGAACCTTTGGAGAAACACGCTGTAATAAACCCTAAG	1356
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Qy	1357	ACGTTGGTGTCTCTGTGGTAACTGTAGCAATTTTCAACCGGACACCGTGTGTCCGGA	1416
Db	647	ACGTTGGTGTCTCTGTGGTAACTGTAGCAATTTTCAACCGGACACCGTGTGTGTCCGGA	706
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Db	707	TGGTGTATTAACCATTAACAAGATGAGAGGGAACAATCTTAGTTACAACCTTGGAGGAGATGG	766
Qy	1477	GATGTTCGGCTGGAATCATAGCTATTGATCTTCTGTGTACATGCTTCAGTGTAAACCTTA	1536

Db 767 GATGTCGCGTGAATACATACATATGATCTGCTGATGACATCTTCACTAACCCTA 826
QY 1537 ATAGTATGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1596
Db 827 ATAGTATGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 886
QY 1597 ACAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1656
Db 887 ACAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 946
QY 1657 CTACCGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1716
Db 947 CTACCGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1006
QY 1717 ATAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1776
Db 1007 ATAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1032
QY 1777 AATCTCTGACCGACCTAGTAACTAATTTGTTGTTTGGATGATGATGATG 1836
Db 1033 -----AGAGTCTGTACACAGAG 1051
QY 1837 AAGTGAACAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1896
Db 1052 AAGTGAACAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1111
QY 1897 AAGCTCAAGACAAATCACTACTAGTCTGCTGCTGCTGCTGCTGCTGCTG 1956
Db 1112 AAGCTCAAGACAAATCACTACTAGTCTGCTGCTGCTGCTGCTGCTGCTG 1171
QY 1957 TTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2016
Db 1172 TTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
QY 2017 CCACCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2076
Db 1232 CCACCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1291
QY 2077 ATCTGTCCAAAGCCATGATCCCGGACTACAGATGCTGCTGCTGCTGCTG 2136
Db 1292 ATCTGTCCAAAGCCATGATCCCGGACTACAGATGCTGCTGCTGCTGCTG 1351
QY 2137 CGGCAAGCAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2196
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QY 2257 ATGATGCTGCTTACATGATGATGATGATGATGATGATGATGATGATGATG 2316
Db 1472 ATGATGCTGCTTACATGATGATGATGATGATGATGATGATGATGATGATG 1531
QY 2317 TCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2376
Db 1532 TCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1591
QY 2377 AGAGGCCAACGAGAACAACTCTGGGCTGATGATGATGATGATGATGATG 2435
Db 1592 AGAGGCCAACGAGAACAACTCTGGGCTGATGATGATGATGATGATGATG 1650

RESULT 2
US-08-066-299-11
Sequence 11, Application US/08066299
Patent No. 5445947
GENERAL INFORMATION:
APPLICANT: James George Metz
APPLICANT: Kathryn Dennis Lardizabal
APPLICANT: Michael W. Lassner
TITLE OF INVENTION: Fatty Acyl CoA: Fatty Alcohol
TITLE OF INVENTION: O-Acyltransferases

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/066,299
FILING DATE: 19930520
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/796,256
FILING DATE: 20-NOVEMBER-1991
APPLICATION NUMBER: 07/933,411
FILING DATE: 21-AUGUST-1992
APPLICATION NUMBER: PCT/US92/09863
FILING DATE: 13-NOVEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: CGNE 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-066-299-11

Query Match 10.7%; Score 296.8; DB 1; Length 1783;
Best Local Similarity 55.2%; Pred. No. 2,1e-56;
Matches 735; Conservative 0; Mismatches 447; Indels 150; Gaps 2;

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Db 389 ACGAGATGTTATGATGATGATGATGATGATGATGATGATGATGATGATG 448
QY 1186 TCAAGAGAGGATCTTCAAGCCCTCAGGATAGGCGAGACATAGCTCCCAAGATCA 1245
Db 449 TTCAAGAGAGGATCTTCAAGAGGCGGATAGGCGGAGAACTAGCTCCCAAGATCG 508
QY 1246 TCTGTTTCAAGAAACATTAACAAGATGAAGAAGTCTGAAGAAGCTCTACAGTGA 1305
Db 509 TCATTAAGGTCGCCCGAGCCGAGCATAGCAGCAGCAGGCGGAGGAGGATGTA 568
QY 1306 TCTTTGAGACACTAGAGCAACTCTTCAGAGAGACAGAGTAAACCTAAAGAGCTGTG 1365
Db 569 TGTAGGGGGCATGACGAGAGGTGTGGAGAGAGGGGGGTGAACCCGACAGATAGGAA 628
QY 1366 TCTTTGAGTAACTGATGATGATGATGATGATGATGATGATGATGATGATG 1425
Db 629 TACTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 688
QY 1426 ACCATTACAGATGAGAGGAGCAATTAATTAACAACCTTGAGAGGATGGATGTTGCG 1485
Db 689 ACCATTACAGATGAGAGGAGCAATTAATTAACAACCTTGAGAGGATGGATGTTGCG 748
QY 1486 CTGGAATCATAGCTATGATGATGATGATGATGATGATGATGATGATGATG 1545
Db 749 CTGGGCTCATTTCCATGATGATGATGATGATGATGATGATGATGATGATG 808

```

OY 1546 CTGTTGTTGAGTACTGAGATGTTGGGTATATATGTTACGTGGAGAGTACAGTCAA 1605
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 809 TGTATGTTAGTACGACAGAAAACATACCTTATTTGTTAGTGGGCAATGACCGTCCA 868
OY 1606 TGGTATATACCTAATTTCTTTCTTTAGGATGGTTGTTCTGCCGTTATGCTCTACCCGTC 1665
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 869 TGGTATATACCAACTGCTATTTTCCATGCGTGGGCGCCGATCATCTCTCTCAACCGGT 928
OY 1666 GTGCTGACTTTGGCCATGTTAGTACCGTCTGAGACATTTGCCAATCATTAAGGCTG 1725
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 929 GGGCTGATGTCGCCGATCCAGTACCAACTCTCTTCACACAGTACCACCCCAAGGCGG 988
OY 1726 CTGACGACCGTGAAGCTTCAGGTTTCATTTTGTATTAATTCGTTTACATCTCTTG 1785
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 989 CTGACGAC----- 996
OY 1786 ACCGACCTGAATAATTTTGTGTTTATGAGTGTATACGAGAGAAAGATGAAC 1845
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 997 -----AAGTCCATATGATGCGCTTACAAACAAGAGATGA 1033
OY 1846 AAGGATTCAGGGGTTGAAGATAGTAGAGACTTATGAGATTTGAGGTGAAGCTCTCA 1905
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1034 ATTAACAGGTAGGTGTTGCTTATCCAGAGATCTGATGCGAGTTGCCGGTGAAGCCCTTA 1093
OY 1906 AGACAAACATCACTACCTTAGGTCCTGCTCTCTACCTTTCTCCGAGAGCTCTCTCT 1965
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1094 AGCCCAACATCAACAGACCTTGGTCCCTCTGCTGCTCCCATGTGAGAACACTCTCTCT 1153
OY 1966 TTGCTGCTTTGCTCCGCGCAACATTTCTCACTGCTGCCAAACGTCACAAACCACTCT 2025
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1154 TTGCGCACTTATGAGCAGCTAAGTCTTCAAGATGACGAACGTG----- 1197
OY 2026 TCTCTACTTCCGCGACCGCAAAACCAATGGAATCAAGTCTCTCTCTCGATCTGCCA 2085
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1198 -----A 1198
OY 2086 ACCATACATCCCGGACACTCAAGCTGCGCTTGCAGCATTTTGTCCACGCGGCAAGCA 2145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1199 AGCCATACATCCCGGACACTTCAAGTGTGCGACGAGCACTTCTCATCTCATGACGAGGCA 1258
OY 2146 AAGTACTGCTTGAAGAGCTTCAAAAGATCTAGGCTTGAAGTGAAGAAATATGAGGCTT 2205
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1259 AAGCACTGTTGATGATGCTGAGACGAACTTGAAGTGAAGGCACTTGAAGCTTGAAGCC 1318
OY 2206 CTAGATGACACTTCAAGCTTGAAGAACTTCAAGCTTGAAGTGAAGTGAAGTGAAGT 2265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1319 CGAGGATGACACTGTATAGGTTGGGAAACATCGAGTACCTTATGATGAGAGTGG 1378
OY 2266 CTACATGAGGCGCAAGAAAGTGTGCTGAGAGCGCATGAGGTTTGGCAGATGCTTGG 2325
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1379 CATACGCTGAACCAAAAGGAGGATCCGTAAGGCTATGCACTTGAAGTGAAGTGAAGT 1438
OY 2326 GTTCTGTTTTAAGTGAACAGTGTGCTGGAAGCAATGAGGAAGTGAAGCAAGCCAA 2385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1439 GTTCAAGTGTCAAGTGTACAGTGTGTGTGAGGCTTGAAGTGAAGTGAAGTGAAGT 1498
OY 2386 CCAGGAACAATCTGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1499 GAGAGAGAGATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1558
OY 2446 TTCTCTTAATTT 2457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1559 CACCTATGCTT 1570
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 3

US-08-265-047-3

Sequence 3, Application us/08265047

Patent No. 5679881

GENERAL INFORMATION:

APPLICANT: Metz, James G.

APPLICANT: Iardizabal, Kathryn D.

```

APPLICANT: Lassen, Michael
TITLE OF INVENTION: Nucleic Acid Sequences Encoding a Plant Cytoplasmic Protein
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,047
FILING DATE: 23-JUN-94
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/160,602
FILING DATE: 30-NOV-93
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/796,256
FILING DATE: 20-NOV-91
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/933,411
FILING DATE: 21-AUG-92
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/066,299
FILING DATE: 20-MAY-93
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09863
FILING DATE: 13-NOV-92
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 101-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-265-047-3
Query Match 10.7%; Score 296.8; DB 1; Length 1783;
Best Local Similarity 55.2%; Pred. No. 2.1e-56;
Matches 735; Conservative 0; Mismatches 447; Indels 150; Gaps 2;
OY 1126 AAGAAGATTATAGAACTAGACGAGAAATACAGGAAGTTGACGAGAGACACTGCTT 1185
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 389 ACAGAGATGTTCAATGACCGGACCTCCCGGCGGTCGTTTCTTAAGAGAAATATGAGT 448
OY 1186 TCAAGAAGAGATCTTACAAAGCTTCAGGCTATAGCGCAGACAGATACGTTCCAAAGTCCA 1245
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 449 TTCAAGAGAGATCTTGAAGAGGCGGATGATGGCCGGAACCTACGTCGCCGAATCCG 508
OY 1246 TCTCTTCATCAGAAAACATTAACAGATGAAGAGAGTGTGTAAGAGAGCTCTACAGTGA 1305
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 509 TCACCTAAGTGGCGCCCGGACCGAGCATATGACACAGCCAGGCGGAGGAGAGAGTGA 568
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1306 TCTTTGAGCACTAGACGAACCTTTCAGAGAAAGACAGTGTAAACCTTAAGAGCTTGGTG 1365
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY	1793	TAGTAACATAATTTTGTGTGTTTGTAGAGGTGGTACCGAGAAAGAAAGTGAACAAAGATT	1852
Db	996	-----TAAAGCTTTCCGTGTGTGTTTATCAAGAGCAGAGTATACAGGAG	1040
QY	1853	CAAGGGGTGAGATAGTATGAGACTTAAATGGAAGTTGAGAGGTGAAGCTCTCAAGCAAA	1912
Db	1041	AACGGGCGTTTGTGTGTCGAAAGATCTAATGGGAGTGAAGGAGAACTCTCAAAACCA	1100
QY	1913	CATCACTACTTATAGGTCTCTTGTCTTACCCTTTCTCCAGACAGCTTCTCTTGTGTCG	1972
Db	1101	TATCACTACTTATAGGTCTCTTGTCTTACCAGTAAAGTGAAGCAGATATCTCTCTTT	1155
QY	1973	TTTGTCTCCGCGCAATCTCACTCTGTCGCAAAAGCTCAACAACACTCTCTCTAC	2032
Db	1156	-----	1155
QY	2033	TTCCGCCACGCAAAAACCAATGGAATCAAGTCTTCCTCTCCATCTGTCCAAACCTA	2092
Db	1156	-----ATGACTCTAGTTGTGGAAGAGCTTTTAACGGTTAAAGTGAACCGTA	1202
QY	2093	CATCCGGACTACAGCTGCGCTTGAGATTTTGCTTCCACGGCGCAAGCAAGTGT	2152
Db	1203	TATCCGGATTTCAAACTGTCTTGAGAGATTTCTGTATCCATGCTGTGGAAGGCTGT	1262
QY	2153	GCTTGAAGAGCTTCAAAAGATATCTAGGCTTGAAGTGAAGATATGAGAGCTTCAAGAT	2212
Db	1263	GATCGATGATTTAGAGAAAGATGTGACGCTTTCACACAGTCAATGTTCAGAGCTTGAAGAT	1332
QY	2213	GACACTTCAAGGTTTGGAAACACTTCTAGCAGTGAATCTGTATGAGTTGGCTTACAT	2272
Db	1323	GACTCTTCATCGATTTGGTGAACACTTCTCGAGCTCCATTTGGTATGAAATGGCTTACAT	1382
QY	2273	GGAGGGCCAAAGAAAGTGTGCTGAGAGCGATAGGGTTGGCAGATACGCTTTCGTTGCG	2332
Db	1383	TGAAGCCAAAGGAAGGTGGGAAGAGATATGCTGTGTTGGCAAAATCGCTTGGGAAGTG	1442
QY	2333	TTTTTAAGTGAAGTGTGTGTGGAAGCAATGAGAAAGTGAAGAAACCAACCGAGAA	2392
Db	1443	ATTTAATATGTAATAGCGCGATTTGGGAACATTAAGCGATGT---GAAACCTTGAACAA	1499
QY	2393	CAATCTCTGGGGGTGATTCATCAACCGTTAACCTGTGCTCT	2434
Db	1500	CAGTCTCTGGGAAGATTGTATTCACAAGTATCCGGTAACTTT	1541

RESULT 5
 US-08-066-299-10
 Sequence 10, Application US/08066299
 Patent No. 5445947
 GENERAL INFORMATION:
 APPLICANT: James George Metz
 APPLICANT: Kathryn Dennis Lardizabal
 APPLICANT: Michael W. Lassner
 TITLE OF INVENTION: Fatty Acyl CoA: Fatty Alcohol
 TITLE OF INVENTION: O-Acyltransferases
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Calgene, Inc.
 STREET: 1920 Fifth Street
 CITY: Davis
 STATE: CA
 COUNTRY: USA
 ZIP: 95616
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 6.0.7
 SOFTWARE: Microsoft Word 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/066,299
 FILING DATE: 19930520
 CLASSIFICATION: 435

```

1      PRIOR APPLICATION DATA:
2      APPLICATION NUMBER: 07/796,256
3      FILING DATE: 20-NOVEMBER-1991
4      APPLICATION NUMBER: 07/933,411
5      FILING DATE: 21-AUGUST-1992
6      APPLICATION NUMBER: PCT/US92/09863
7      FILING DATE: 13-NOVEMBER-1992
8      ATTORNEY/AGENT INFORMATION:
9      NAME: Elizabeth Lassen
10     REGISTRATION NUMBER: 31,845
11     NAME: Donna E. Scherer
12     REGISTRATION NUMBER: 34,719
13     REFERENCE/DOCKET NUMBER: CNE 98
14     TELECOMMUNICATION INFORMATION:
15     TELEPHONE: (916) 753-6313
16     TELEFAX: (916) 753-1510
17     INFORMATION FOR SEQ ID NO: 10:
18     SEQUENCE CHARACTERISTICS:
19     LENGTH: 1733 base pairs
20     TYPE: nucleic acid
21     STRANDEDNESS: double
22     TOPOLOGY: linear
23     MOLECULE TYPE: CDNA to mRNA
24     OS-08-066-299-10

```

	Query Match	9.9%	Score 275.4	DB 1	Length 1733	
	Best Local Similarity	54.6%	Pred. No. 1,1e-51			
	Matches 729	Conservative	0	Mismatches 453	Indels 153	Gaps 3
QY	1126	AAGAAGCTTCATAGACACTACCGAGAAAATCAGGGAAGTTGACGAGAGACACTCGGTT	1185			
Db	424	ACGAGATGTTATGAGACCGAGACTCCCGGGCGGGCTTTCTTAAGGAAATATAGAT	483			
QY	1186	TCAAGAAGAGGTCTTTACAAAGCTCAGGATATGGGAGACGACATATACGACCAAGATGCA	1245			
Db	484	TTCAAGAGAGATCTTTGGAGAGGGCCGGTATGGGTGCGGAAACCTATGTCCCGAATCCG	543			
QY	1246	TCTCTTCATCAGAAAACATTAACACAGATGAAAAGAGTGTGAAAGGCTCTACAGTA	1305			
Db	544	TCACATAAGGTGCCCCCGCCGACGACATAGCAGACCCAGGGCCGAGGGAGAGAGTGA	603			
QY	1306	TCTTTGAGGACATACGAAACCTCTCGAAGACACAGTCGTAAAAACCTAANAAGCTGGTG	1365			
Db	604	TGTACGGGGCGATCGACGAGGTGTGGAAACACGGGGGTGAAGCCGAACGACATGAGAA	663			
QY	1366	TCTCTTGTTAACTAGTATGACATTTTCAACCCGACACCGCTGTGTGCCAGATGGTGATA	1425			
Db	664	TACTGTGTGTGANTGACAGCTGTTTAAACCAAGCGCCGTGCTCATCATGATAGTTA	723			
QY	1426	AACATTAAAGATGAGAGGAACATATCTTAAGTTACAACTTGGAGGATGGCATGTTCGG	1485			
Db	724	ACCATTTAAGCTNAGGGGTATATACCTTAAGTATATTTGGTGGCAAGGTTGGAAGTG	783			
QY	1486	CTGGAATCATAGACATTTATGATCTGCTCGGACATGCTTACGTACACCT---AATAGTT	1542			
Db	784	CTGGGCTCATTTCCATTGATGTCCTGGCAAGGACCTCCTACAGGTTTACGTTAAAAACAT	843			
QY	1543	ATGCTGTGTTGTGAGTACTGAGATGTTGGGTATATATTGTAACGTGGGAGAGTGACAACT	1602			
Db	844	ATGTGTTAGTGTAGTGACACGGAACATGACCCCTTAATTGTAACGTGGGCAATGACCGCT	903			
QY	1603	CAATGTTATTAACCTAATTTGTTCTTAAAGATGGGTGTTCTGCGGTTATGACTCTACACC	1662			
Db	904	CCATGCTTATACCAACACTGCTATTTTCGATGGGTGGCGCTGCATCATCTCTCTCAAGC	963			
QY	1663	GTCGTGCTGACTTTCGCAATGCTAAGTACCGCTCTCGAGCACATTGTCCGAATCATTAAG	1722			
Db	964	GCTGGCGGATGCTGCGCGGATCCAAAGTACCAACTCCTTCATACAGTAGACACCAACAAG	1023			
QY	1723	CTGCTGACGACCGTACGTTCAAGTTCAATTCATTTGGTATTAATTTGCTTTTACAATCTC	1782			
Db	1024	GCGGTGAGAC-----	1034			


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OY 1603 CAATGGTTATACCTAATTGTTCTTTAGATGGGTTGTTGCGGTTATGCTCTACACC 1662
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DB 904 CCAATGCTTATACCACTATTTGCGATGGGCGGCTGCAATCCCTCAACACC 963
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OY 1663 GTCGTCGTACTTCCGATCTAAGTACCGCTCTGACACATTTGCCAATCTAAGG 1722
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 964 GCTGGCGTATGTCGCGGATCAAGTACCAATCTCTCATACATAGACGCCAAGG 1023
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1723 CTGCTGACGACCGTACGTTCAAGTTTCAATTTGTTAATTTGCTTTTACATCTC 1782
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1024 GCGCTGAGAC----- 1034
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1783 TTGACCGACTAGTAATAATTTGTGTTTGAAGATGTGACAGAGAGAAG 1842
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1035 -----AAGTCTATAGATGGCTTTTACACAGAGAAG 1068
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1843 AACAGGATTCAAGGGTTGAAGTAACTAGACACTTAATGGAAGTTGAGGTGAAGCTC 1902
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1069 AAAATTAACAGTAGTGTCTTATCCAAAGATCTGATGGCACTTGCCGGTGAAGGCC 1128
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1903 TCAGACAAATACATCTACTAGTCTCTTCTCTACCTTTCTCCGACAGCTTCTCT 1962
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1129 TAAAGGCCAATACGACGCTTGTGCTCCCTGCTCCCATGTCAAGACAACTCTCT 1188
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1963 TCTTTGCTGTTTGTCCGCGCAACATCTCAACCTGTCGCAAAAGCTCAACACACTT 2022
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1189 TCTTTGCGACCTTATGTGCGACGATAGCTTCTCAAGATACAGACGCTG----- 1235
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2023 CCTTCTACTTCCGCCACCCCAAAACCAATGGAATCAAGTCTCTCTCCGATCTGT 2082
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1236 ----- 1235
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2083 CCAAGCCATATACCCGACTCAAGCTCGCTTGACATTTTGTCTTCCACGGGCA 2142
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1236 --AAGCCATATACCCGACTTCAAGTGTGCGACGACGACACTTCTGCAATCCATGCAAGAG 1293
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2143 GCAAGTACTGCTGAAGAGCTTCAAAAGAACTAGGCTTGAGTGAAGAGATATAGAGG 2202
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1294 GCAAGGAGTGTGATAGCTCGAAGAACTTGAGCTTGAAGCCATGCACTTGAAC 1353
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2203 CTCTAGAGTACACTTCAAGTTTGAACACTTCTAGACAGTGAATCTGTATAGAT 2262
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1354 CCTGAGATGACACTGATATAGTTTGGGAACATCGATGATTAATGATGAGAT 1413
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2263 TGGCTTACATGAGCCCAAGAAAGTGTCTGAGAGCGATAGGCTTTGGCAGATCGCTT 2322
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DB 1414 TGGCATAGCTGAAGCAAAAGGAGGATCCGTAAAGGTGATCGAATCTTGATGAT 1473
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OY 2323 TCGGTTGCTTTAAGGTGAAGAGTGTGTTGGAAGCAATGAGGAAGGAAAGAC 2382
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1474 TTGGTTAGGTTTCAAGGTGAACAGTGTGTGAGAGGCTTTGAGAGGTGCAATCCGG 1533
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2383 CAACAGGAAACATCTTGGGTGATGATGATCAACCCCTGCTCTCTAAATTA 2442
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1534 CTAGAGAGAAATCCTTGATGATGAATTAAGAACTTCCCTGCTCATGCTTAAAA 1593
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 2443 TCATTTCTTAAT 2457
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1594 TCGCACCTATCGCTT 1608
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```

```

RESULT 7
US-08-926-522-21
; Sequence 21, Application US/08926522
; Patent No. 6426447
; GENERAL INFORMATION:
; APPLICANT: Vlc C. Knauf
; APPLICANT: Gregory A. Thompson
; TITLE OF INVENTION: PLANT SEED OILS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.

```

```

STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1(a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,522
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,173
FILING DATE: 2-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schmedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE DES
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1733 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-926-522-21

Query Match 9.9%; Score 275.4; DB 4; Length 1733;
Best Local Similarity 54.6%; Pred. No. 1.1e-51;
Matches 729; Conservative 0; Mismatches 453; Indels 153; Gaps 3;

OY 1126 AAGAAGACTTATAGACATAGCGAGAAATACAGGAAGTTGCGACGAGACACTCGGTT 1185
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 424 ACGAATATTTATAGACCGGACCTCCGCGCGGCTGCTTTCTAAGGAAATATTGAGT 483
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1186 TCAGAAAGAGATCTTACAGCTTACGACATAGGCGACGACATACGCTCCCAATGCA 1245
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DB 484 TTCAGAGGAAGATCTTGAAGAGGCGCGGATGGTTCGGGAAACATATGCTCCGATCCG 543
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1246 TCTCTTCATCAAAACATACACAGATGAAGAGTCTGTAAGAAAGCTCTACAGTGA 1305
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 544 TCACTAAGGTGCGCCCGACCGACATACGACGACGCGGCGGAGGAGGTGA 603
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1306 TCTTTGAGCACTAGACAACTCTTGCAGAGACAGTGTAAACCTTAAGAGCTTGTG 1365
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 604 TGTAGGGGCGGATGACAGAGTGTGGAAGAACGCGGGGTGAAGCGGAAGATAGGA 663
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1366 TCTTTGTTAATCTGATTTTCAACCCGACACCGTGTGTCGCAATGTGATTA 1425
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 664 TACTGTGTGANTGACAGCTTGTAAACCAACCGCGCTGATCATCATGATAGTTA 723
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1426 ACCATTACAGATGAGAGGAACATCTTATGTTACACCTTGAGAGGATGGATTTGG 1485
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 724 ACCATTACAGCTNAGGGGTAATATATAGTAAATCTTGTTGGATCTTCAAGT 783
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1486 CTGAATCATAGATATGATCTTGTGTCGATGCTTCAAGTCAAGTCAAGTCAAGT 1542
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 784 CTGGGCTCATTTCCATGATCTTGTGCAAGAGACCTCTTACAGGTTTACGCTAAAAACAT 843
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1543 ATGCTGTTGTGAGTACTGATGATGTTGGTATTAATTTGTAAGTCAAGTCAAGT 1602
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 844 ATGCTAGTAGTAGACAGGAAACATGACCTTAATTTGTAAGTCAAGTCAAGTCAAGT 903
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OY 1603 CAATGTTATACCTAATTTGTTTGTAGAGTGGTGTCTGCGCTTATGCTCTAAC 1662
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Db 904 CATGCTTATACCAACATGCTATTTTGCATGGTGGCGCTGCATCATCTCTCAAAC 963
OY 1663 GTCGTCGTACTTGGCCATGCTAGTACCGTCTGAGACATTTGTCGAACCTCATAG 1722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 964 GCTGGGTATGCTGCTCCATCCAACTGATACCACTCTTATACAGTACGACCAACG 1023
OY 1723 CTGCTGACGACCGTACCTCAGGTTTCATTCAATTTGGTATTAATTCGTTTACAATCTC 1782
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1024 GGGCTGACGAC----- 1034
OY 1783 TTGACCGACTAGTAATTTTGTGTTTGTAGAGTGTGTCAGAGAGAGAG 1842
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1035 -----AACTCTATAGATGCTCTTACACAGAGAGATG 1068
OY 1843 AACAGGATTCAGAGGTTGAAGATTAAGTACCTTAATGGAAGTGGAGTGAAGCTC 1902
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1069 AAAATACAGAGTATGTTGCTTATCCAAAGATCTGATGACAGTGGCGGTAAGCCC 1128
OY 1903 TCAGACAAACATCACTACTAGGCTCTGTCTACCTTCTCCGACGCTTCT 1962
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1129 TAAAGGCCAATCACAGACCTTGTCTCCCTGCTGCTCCATGTACAGAACACTCTCT 1188
OY 1963 TCTTGTGCTTGTCTGCGCGAACATCTCTACCTGCTGCCAAAGCTCAACACACTT 2022
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1189 TCTTGGCACCCTTACTGACAGCTAGGCTCTCAAGATGACGAACGTG----- 1235
OY 2023 CTTCTCTACTTCCGCGCAACCGAATAACCAATGGAATCAAGTCTTCTCCGATCTGT 2082
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1236 ----- 1235
OY 2083 CCAAGCATACATCCGCGACTACAGCTCGCTTCAGACATTTTGTCCAGCGGGCA 2142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1236 --AAGCCATATATCCCAATTTCAAGTGGCAGCAGACACTTCTCATCCATGACAGG 1293
OY 2143 GCAAGTGTGCTTGAAGAGCTTCAAAAGAACTAGGCTTGAAGTGAAGATATGAGG 2202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1294 GCAAGGAGTGTGATGATGCTCGAAGAACTTGAAGTGAAGCAGCGCATGGCACTTGAAC 1353
OY 2203 CTTTAGAGTACACTTACAGGTTTGAACACTTCTAGACAGTGAAGTGTGATGAGT 2262
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1354 CTTGAGATACACTGTATAGTGTGGAACACATCGAAGTCTCAATTAATGTCAGAGT 1413
OY 2263 TGGCTTACATGAGGAGCCAAAGAGTGTCTAGAGCGGATAGGTTTGGAGATCGCT 2322
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1414 TGGCATAGCTGAAGCAAAAGAGAGATCCCTAAGGATGATGCAATCTTGATGATGAT 1473
OY 2323 TCGGTTTGTGTTTAAGTGAAGTGTGCTGGAAGCAATGAGAAAGTGAAGAGC 2382
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1474 TTGGTTAGGTTTCAAGTGAAGTGTGCTGAGAGGCTTTGAGGAGTCAATCCG 1533
OY 2383 CAACGAGAACATCTTGGTGGATGATGATCAACCGTACCGTGTGCTCTTAATTA 2442
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1534 CTAGAGAGAAATCTTGGATGATGAATGAGAAATGCCGTCTCATGTCCTAAAA 1593
OY 2443 TCATTTCTTAATTT 2457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1594 TCGACCTATCGCTT 1608
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RESULT 8
US-08-868-373-1
; Sequence 1, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beltemmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868,373
; CURRENT FILING DATE: 1997-06-03

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; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-08-868-373-1

Query Match      9.7%; Score 269; DB 4; Length 1560;
Best Local Similarity 55.2%; Pred. No. 2.7e-50;
Matches 723; Conservative 0; Mismatches 430; Indels 156; Gaps 4;

OY 1123 CAAGAGAGTTCATAGTACGAGAGAAATCAGGAAAGTTCGACGAGACACTCG 1182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 392 CAGTATATCTGTTCTTGAAGATGACGAGAGAAATGATCATCATCCATGACAGCTTC 451
OY 1183 GTTTCAGAGAGAGATCTTCAAGGCTCAGCATAGCCACGACGATATCGTCCAAAGT 1242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 452 AGTTCCAGAGAGAGATCTTGAACCGGCGGTTGGAGACGAGAGCTATCTGCCACGTG 511
OY 1243 CCATCTCTCATCAGAGAAACATACACGATGAAGAGTGTGAGAGAGCTCTACAG 1302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 512 GCATACCTTCAACGCGCCCGGAGGCTAATATGTACAGGACGCTGCGAAGCTGAAGCCG 571
OY 1303 TCATCTTGGACACTACAGCAAGCTCTTGGAGAGACAGTGTAAACCTTAAGACGTTG 1362
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 572 TTATGTGTGAGACCTTGAATTCCTCTTCGAGAGAAACCGGAATTAACCGCGCAAGTCG 631
OY 1363 GTGTCTTGTGTGATAGTATGATCTTCAACCGGACCGGCTGTGTCGGAATGATGCA 1422
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 632 GAATCTTATATGATTAAGTACGACCTTATTAATCCAGCGCTCTATAGGATGATCG 691
OY 1423 TAAACCATTAAGATGAGAGAGAAACATTAAGTTACAACTTGGAGGATGATGTT 1482
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 692 TGAACCATTAAGATGAGAGAGAAACATTAAGTTACAACTTGGAGGATGATGTT 751
OY 1483 CGGCGGAATATACCTATTAATCTGCTCGGACATGCTTCAAGCTTAACCTTAAGTT 1542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 752 CGGCGGAATATTAATCTGCTCGGACATGCTTCAAGCTTAACCTTAAGTT 811
OY 1543 ATGCTGTGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1602
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 812 ACGCTGTGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 871
OY 1603 CAATGTTATACCTAATTTGTTTGTAGAGTGGTGTGCTTCCGTTATGCTCTTAAC 1662
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 872 CAATGCTCTCTGCAACGATCTTCCGATGAGGAGGAGTGTGCTTCCGTTATGCTCTTAAC 931
OY 1663 GTCGTCGTACTTTCGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 1722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 932 GCCGTCAAGACCGGAGAGAAAGTCAAGTCTGCTGTCGATGATGATGATGATGATGAT 991
OY 1723 CTGCTGACGACCTAGCTTCAAGTGTTCATTCATTTTGGTATTAATGTTTACAATCTC 1782
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 992 GATCAGACGACAAACTACATTT----- 1015
OY 1783 TTGACGACCTAGTAAATTTTGTGTTTGTAGAGTGTGTACGAGAGAGATG 1842
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1016 -----GGGTGTACAGAGAGAGAG 1036
OY 1843 AACAGGATTCAGAGGTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1902
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1037 AGAGAGAGAAATCTGCTCTTCTTACTAGAGGCTATGATGCTGCGGAGAGACCTG 1096
OY 1903 TCAAGACAAACATCACTACCTTAGAGTCTTGTGCTACCTTCTGAGAGAGTCTCT 1962
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1097 TGAAGAGAAACATCACTACCTTAGAGTCTTGTGCTACCTTCTGAGAGAGTCTCT 1156
OY 1963 TCTTGTGCTTGTGCTGCGGAGAACTTCACTGCTGCAAAAGCTCCACAACCACTT 2022
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1157 TCTTGTATTCCTTGTGTC----- 1173
OY 2023 CTTCTCTACTTCCGCGCAACCGCAAAACCAATGGAATCAAGTCTTCTCTCCAGTCTGT 2082
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 1174 -----AAAGAGATGTTCAAGTAAAGT----- 1200
QY 2083 CCAAGCATACATCCGAGTACAAAGCTGCGCTTCGACATTTTGGCTTCACGCGGCA 2142
Db 1201 --AAACCTAATATCCGATTTCAAGTAGCTTTGACGATTTCTGTAATTCAGAGAG 1258
QY 2143 GCAAGTAGTGCTTCAAGAGCTTCAAGAAATCTAGGCTTGATGTAAGAAATAGAGAG 2202
Db 1259 GTAGAGCGGTTTACAGCAAGTGCAGAAATCTGATCTCAAAAGATTGGCCATAGAAC 1318
QY 2203 CTTAGAGTACATCTTACAGAGTTCGAAACACTTTCAGACGTAATCTGATAGT 2262
Db 1319 CTTAGATGATGCTTTCAGACAGATTTGTAACACTTCGATGCTGCTTTCGATGAGA 1378
QY 2283 TGGCTTACATGAGGCGCAAGAAAGTTCGTAGAGCGGATAGGCTTGGCAGATCGCT 2322
Db 1379 TGGCTTATACCGAAGCTAAGGCTCGGTTAAAGCTGACCGACTTGGCAGATTCGCT 1438
QY 2323 TCGGTTCTGTTTAAAGTAACTGCTGTGTGAGAGGCAATGAGAAAGT---GAGA 2379
Db 1439 TTGATCGGTTTCAAGGTATATATGCGGTTTGAAAGCGTTACACCGGTTTCGACGG 1498
QY 2380 AGCCAAACAGAGAAACATCTTGGGAGTTCATCAACCGTACCTGT 2428
Db 1489 AGGAGATACCGGTAATGCTTGGCTGCTGATTCATCATATCCGCT 1547

RESULT 9
US-08-868-373-9
: Sequence 9, Application US/08868373
: Patent No. 6307128
: GENERAL INFORMATION:
: APPLICANT: Javoriski, Jan G.
: APPLICANT: Post-Belienmiller, Martha A.
: APPLICANT: Todd, James
: TITLE OF INVENTION: FATTY ACID ELONGASES
: FILE REFERENCE: 07148/064001
: CURRENT APPLICATION NUMBER: US/08/868,373
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 9
: LENGTH: 1611
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-08-868-373-9

Query Match 9.68; Score 268.4; DB 4; Length 1611;
Best Local Similarity 54.5%; Pred. No. 3.6e-50;
Matches 722; Conservative 0; Mismatches 446; Indels 156; Gaps 3;

Db 740 CATATATTGTTAAACAAGTATTAAGCTTAGAGGAAATGTTAAAGTTCATGCTGGA 799
QY 1474 TGGAGTGTTCGGCTGGAATCATATGATATGATCTGCTGACATGCTTCAAGTAAAC 1533
Db 800 TGGGATGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 859
QY 1534 CTAAATGTTATCTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1593
Db 860 GGAATACCTATGCTGTTGGTTAGTACGAAACATTAAGTAAAGTATGATGATGATG 919
QY 1594 GTACAAAGCATAGGTTATATCTAATGTTTCTTAGATGAGTGGTGTGCTGCTTATC 1653
Db 920 ATAAAGAGCTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 979
QY 1654 TCTTAACCGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1713
Db 980 TGTGCAACAAAGGGAAGAAATCGTAGCGGCTTAAGTAAATGATGATGATGATGAT 1039
QY 1714 CTATTAAGGCTGCTACACAGCTAGCTTCAAGTTTCAATTTGATTAATTCGTT 1773
Db 1040 CTATTAAGGAGAGCTG----- 1054
QY 1774 TCAATTCCTTGACCGACTAGTAACTAATTTGTGTGTTTTPAGAGTGTATCCAG 1833
Db 1055 -----TTGAGAAAGCTTTCACATGTTTTCACAG 1084
QY 1834 AAGAAGATGAACAGGATTCAGAGGTTGAAAGATTAAGTAAAGTAAAGTAAAGTAAAG 1893
Db 1085 AGCAAGATGATTAATGGAAGACCGGGGTTTCTGTGCAAAAGATTAATGATTAAGCTG 1144
QY 1894 GTAAAGCTTCAAGCAAAACATCACTTACCTTACCTTCTGCTTCTTCTGCTGAGC 1953
Db 1145 GGAAGCTCTTAAGCGAATATCACTTATGCTTGTGCTTGTGCTTCTTAAAGTAAAG 1204
QY 1954 ACCTCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2013
Db 1205 AATTCCTGTTTTCATGACTTG----- 1227
QY 2014 CAACCACTTCT 2073
Db 1228 -----CTTGAAGAAATGTTTAA 1246
QY 2074 CCGATCTGTCAGGATCATATCCGAGCTACAGCTGCTTCGAGCATTTTGTCTTC 2133
Db 1247 ACTGAGCTGAAGCGATATATTCGAGATTCAAGCTTGCATTTCTGATATCC 1306
QY 2134 ACGCGCAAGCAAGTAAAGTGAAGAGCTTGAAGAGCTTCAAAAGATCTAGGCTGAGTGAAG 2193
Db 1307 ATGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1366
QY 2194 ATATGAGGCTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2253
Db 1367 ATGCGAGGATCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1426
QY 2254 GGTATGATGCTTACATGAGGCGCAAGAAAGTGTGATGAGGCTATGAGGCTTGGC 2313
Db 1427 GGTATGATGCTTACATGAGGCTTAAAGGATGAGAAAGAAACCGGCTTGGC 1486
QY 2314 AGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2373
Db 1487 AGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1546
QY 2374 TGAAGAGCAACAGAAATCTTGGGCTGATGATGATGATGATGATGATGATGATGAT 2433
Db 1547 T---CAAGCTCGGTTAGTATGCTGGAACACATGATGATGATGATGATGATGATG 1603
QY 2434 TCTA 2437
Db 1604 TCGA 1607

RESULT 10

US-08-868-373-11
 : Sequence 11, Application US/08868373
 : Patent No. 6307128
 : GENERAL INFORMATION:
 : APPLICANT: Jaworski, Jan G.
 : APPLICANT: Post-Beltemiller, Martha A.
 : APPLICANT: Todd, James
 : TITLE OF INVENTION: FATTY ACID ELONGASES
 : FILE REFERENCE: 07148/064001
 : CURRENT APPLICATION NUMBER: US/08/868,373
 : CURRENT FILING DATE: 1997-06-03
 : NUMBER OF SEQ ID NOS: 22
 : SOFTWARE: FASTSEQ for Windows Version 3.0
 : SEQ ID NO 11
 : LENGTH: 1502
 : TYPE: DNA
 : ORGANISM: Arabidopsis thaliana
 US-08-868-373-11

Query Match 9.08; Score 249; DB 4; Length 1502;
 Best Local Similarity 54.08; Pred. No. 6.6e-46;
 Matches 699; Conservative 0; Mismatches 440; Indels 156; Gaps 3;

QY 1134 TTCTAGACGAGGAGAAATCAGGAGAGTTCGACGAGACACTGCTTCAAGAG 1193
 DB 337 TTCTAGACGAGGAGTTCGCTTTCCTCAAGGACCAAGCTTAAGAGCTGAGTCCAAATG 396
 QY 1194 AGGATCTTCAAGGCTCAGGAGATAGGAGACAGACATACGCTCCAAAGATCCATCTTCA 1253
 DB 397 AGAATCTTGAAGCTTTCGAGGCTGAGAGAGATGCTCCCTCCGCTTATTCATTTAT 456
 QY 1254 TCAGAAAACATTAACAGGAGAAAGAGTGTGAGAGAGCTGACATGATGCTTTGGA 1313
 DB 457 ATTCCTCCACACCAACCATGAGCGGCTGAGAGCGAGCTCAGATGCTTATCTTCAG 516
 QY 1314 GCATAGACGAGCTTTCGAGAGACAGCTGTAACCTTAAGAGCTTGTCTCTGTG 1373
 DB 517 GCCATGAGGAGTTCCTCAAGAAACCGGCTTAAACCTTAAGAGCTGAGATCTTATC 576
 QY 1374 GTTACTGTACATTTTCAACCCGACCGCTGCTGCTCCGATGCTATTAACCATTTAC 1433
 DB 577 GTCAAGCTGCTCTTCTCTCCACACATCGCTCAGTATGCTATCAACAAATAT 636
 QY 1434 AAGATGAGAGGAGACATCTAGTTACACCTTGAGGAGTGGATGTTGGCTGGAATC 1493
 DB 637 AAGCTTGAAGATATATCAAGAGCTTCAATTTCCGGGATGGGCTGACGCGGCTG 696
 QY 1494 ATAGCTATGATCTTGTCTGAGACATGCTTCAACCTTAAGATTTATGCTGTGTT 1553
 DB 697 ATCTCAGTTGATCTAGCCCGGAGCTTCTCAAGTTCATCCCAATTCAAATGCAATATC 756
 QY 1554 GTGAGTACTAGAGTGGTATTAATTTGAGCTGGAGAGTGCACAGTCAATGTTATTA 1613
 DB 757 GTCAAGCAGGAGATCAACGCTTAATTAATCAAGGACAGAGAGCCATGTTGTTA 816
 QY 1614 CCTAATGTTTCTTAGAGGTTGCTGCTGCTATGCTTACCCGCTGCGAGAC 1673
 DB 817 CCAATTTGCTCTCCGATGGGCGGAGCCATACATGTAACCGCGGCTGTGAC 876
 QY 1674 TTTGCGCATCTAAGATCCCTGCTGAGACATGCTCCGAATCAAGAGTGTGAGAC 1733
 DB 877 CGGTGGGAGCAAAATCAAGCTTTCACACCTGCTCGGAGACACCGTGGGCTGAGAC 936
 QY 1734 CGTAGCTTCAAGCTTCAATTTATTTGTTATTAATTCGTTTACATCTTTCGACGACT 1793
 DB 937 ----- 936
 QY 1794 AGTAATAATTTGTGTGTTTAGAGGTGTGACAGAGAGATGAAGAAGATTC 1853
 DB 937 -----AAGTCTTCTACTGTGTCTACGAGAGAGGAAAGAGGACAC 981
 QY 1854 AAGGGGTTGAAGATTAAGTAGACTTAATGAAGTGGAGTGAAGCTCAAGACAAC 1913
 DB 1913 -----

DB 982 GTTGCAATCACTTGTCCAAAGATCTCATGGCCATGCCGGTGAAGCCCTCAAGGCAAAAC 1041
 QY 1914 ATCACTACTAGTGTCTCTTGTCTTCTACTTCTCCAGACACTCTCTCTTCTGCT 1973
 DB 1042 ATCAACCAATATGATGCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1101
 QY 1974 TTGCTCCGCGCAATTTCTACCTGCTGCGCAAAAGCTGCAACACCTTCTTCTACT 2033
 DB 1102 CTAAATCGAGCTTAAAT----- 1118
 QY 2034 TCCGCGACGCAAAACCAATGATCAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2093
 DB 1119 -----CTTCAACCCGAATGAAACCAATAC 1143
 QY 2094 ATCCGGAATCAACCTGCTTCTGAGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2153
 DB 1144 ATACGGAATCAACCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1203
 QY 2154 CTGGAAGCTTCAAAAGATCTAGGCTTGAAGTGAAGAAATGAGAGCTTCTTACT 2213
 DB 1204 ATCGAGAGCTCCAAAGAAATCTTCAACATCAAGAGAAACAGTGAAGCTTCAAGAAATG 1263
 QY 2214 ACATCTCAGGTTTGAAGAACTCTAGCAAGTGAATCTGTATGATGCTTACTATG 2273
 DB 1284 ACATCAATCTGTTTGTATCAACGCTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1323
 QY 2274 GAGGCAAGAAAGTGTCTGAGAGCGATGAGGTTTGGCAGATCGCTTCTGCTTGT 2333
 DB 1324 GAGTCTAAAGGAGAAATGAGAGAGCGATGAGGCTTGGCAAAATCGCTTGGAGTGT 1383
 QY 2334 TTTAAGTCAACAGTGTCTGAGAGGCAATGAGAGGTTGAAGGAAACCAACAGGAAAC 2393
 DB 1384 TTCAAGTCACTGCTGCTGAGAGGTAAGTACCGTACGATGAAGA---CACCTAAGAGAC 1440
 QY 2394 AATCTGAGTGAATGATCAACCGTATCCCTGT 2428
 DB 1441 GGACCATGCTCGATTTGATGACCGCTTACCTGT 1475

RESULT 11
 US-09-058-947A-3
 : Sequence 3, Application US/09058947A
 : Patent No. 6274790
 : GENERAL INFORMATION:
 : APPLICANT: Kunst et al.
 : TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
 : NUMBER OF SEQUENCES: 12
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Klariquist Sparkman Campbell
 : STREET: One World Trade Center, Suite
 : CITY: Portland
 : STATE: OR
 : COUNTRY: USA
 : ZIP: 97204-2988
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Disk, 3.5-inch
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: Windows NT
 : SOFTWARE: Word97 & ASCII
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/058,947A
 : FILING DATE:
 : CLASSIFICATION: 800
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 60/043,831
 : FILING DATE: April 14, 1997
 : ATTORNEY/AGENT INFORMATION:
 : NAME: David J. Baird, Ph.D.
 : REGISTRATION NUMBER: 41,401
 : REFERENCE/DOCKET NUMBER: 5493-50032/DIE

Db	3206	ACATACATGCTTTTGGTAAACAGTCATCTATCTTATCGTTATGTAAGAGAGCTTAGCTAACATC	3265
QY	2274	GAGGCCAAGAAAGTGTTCGTAGAGCGCATAGGGTTGGCCAGATCGCTTTCGGTCTGCT	2333
Db	3366	GAGCTCTAAAGGAGAAATGAGAGAGGCGCATCGCTTTGGCAAAATCGCTTTGGGAGTGCT	3325
QY	2334	TTTAGTGTTAAAGTGTGGTGCTGGAAAGGCAATGAGGAAGGTGAAGAAAGCAACGAGAAC	2393
Db	3326	TTCAAGGTACTCTGCGCGTGTGGAATGATTAACCGTACATTTAAGA---CACCTAAGGAC	3382
Db	3383	GGACCATGGTCGATTTGATATACGACCGTTACCTGT	3417
RESULT 14			
US-08-888-998-1			
Sequence 1, Application US/08888998			
Patent No. 6124524			
GENERAL INFORMATION:			
APPLICANT: JAMES, Douglas W.			
APPLICANT: LIM, Eda			
APPLICANT: KELLER, Janis			
APPLICANT: DOONER, Hugo K.			
TITLE OF INVENTION: PAEL GENES AND THEIR USES			
NUMBER OF SEQUENCES: 8			
CORRESPONDENCE ADDRESSES:			
ADDRESSEE: Townsend and Townsend Kourile and Crew			
STREET: Steuart Street Tower, One Market Plaza			
CITY: San Francisco			
STATE: California			
COUNTRY: US			
ZIP: 94105-1493			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/888,998			
FILING DATE: 07-JUL-1997			
CLASSIFICATION: 800			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 08/329,603			
FILING DATE: 26-OCT-1994			
ATTORNEY/AGENT INFORMATION:			
NAME: Bastian, Kevin L.			
REGISTRATION NUMBER: 34,774			
REFERENCE/DOCKET NUMBER: 12176-004300			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (415) 543-9600			
TELEFAX: (415) 543-5043			
INFORMATION FOR SEQ ID NO: 1:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 1641 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: both			
TOPOLOGY: both			
MOLECULE TYPE: cDNA			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: 1..1641			
OTHER INFORMATION: /product= "PAEL from Arabidopsis"			
US-08-888-998-1			
Query Match 7.5%; Score 210; DB 3; Length 1641;			
Best Local Similarity 53.0%; Pred. No. 2.6e-37;			
Matches 664; Conservative 0; Mismatches 435; Indels 153; Gaps			
QY	1177	CACCGGTTTCAGAAAGAGATCTTCAAGCCGACGAGCATAGGCGAGCATACGTC	1236
Db	365	CGCTGCAATTCCTGAGAGAAATTCAGAGCGTTCAAGCTTAGGTATGAGACGTACAGTC	424

QY	1237	CAAGATCAATCTCTTATCGAAGAAACATFACAAACAGTGAAGAGTGTGAAGAAGCT	1236
Db	425	CTGAGGAGACTCATTACAGTACCAACCGCGGAAGCTTTTGACCGGTGAGAGAGAG	484
QY	1297	CTACAGTCACTTTGGAGAGCTAGACGAACCTGTGAGAAAGACAGTGTAAACCTTAAG	1356
Db	485	AGAAAGTTATCATCGGAGCGCTGAAAAATCTAFTTGAGAACACCAAGTTAACTTGAG	544
QY	1357	ACGTTGGTGTCTTGTGGTTAACTGTAGCATATTTCAACCCGACACCGTGTTCGCCAA	1416
Db	545	AGATTGGTAATACCTTGGTGGAACCTCAAGCATGTTTATCAACTCTCTTGGATCCGCTA	604
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QY	1717	ATAAGCTGCTGACGACCGTAGCTTCAAGTTTCATTTGTTAATTTGTTTAC	1776
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Db	1010	CAACACTTACGAAAAATATAGCAACATTTGGGTCCGCTGTGATTTCTTTAAGCGAAAGT	1069
QY	1957	TTTCCTTTTGGTGGCTTGTGCTCCGCGCAAACTTGCACAGCTGTCCCAAAAGTCCACA	2016
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QY	2017	CCAACTTCTTCTACTTCCGCGCACCGCAAAAAACCAATGATCAAGTCTTCTTCCG	2076
Db	1104	-----TCTAAGGATTAATCAAGCATTAC-----	1128
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QY	2317	TCGCTTTCGGTCTGTTTTAAGTGAACAGTGTGGTGTGGAAGGCATAGAGAAAGTGA	2376

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Db 1335 TTGCTTTAGGATCAAGGGTTTAAGTAAATAGTGGCGGTTGGCTGGCTACGACATGT-- 1412
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Db 1413 -CAAGGCAATCGGCAAAATAGTCCTTGCAACAAATGCAATGCATGCATGATGATATCCGGT 1463

RESULT 15
US-09-362-633-1
: Sequence 1, Application US/09362633
: Patent No. 6184355
: GENERAL INFORMATION:
: APPLICANT: JAMES, Douglas W.
: APPLICANT: LIM, Eda
: APPLICANT: KELLER, Janis
: APPLICANT: DOONER, Hugo K.
: TITLE OF INVENTION: FAEI GENES AND THEIR USES
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourile and Crew
: STREET: Steuart Street Tower, One Market Plaza
: CITY: San Francisco
: STATE: California
: COUNTRY: US
: ZIP: 94105-1493
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/362.633
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/888,998
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Bastian, Kevin L.
: REGISTRATION NUMBER: 34,774
: REFERENCE/DOCKET NUMBER: 12176-004300
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 543-9600
: TELEFAX: (415) 543-5043
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1641 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..1641
: OTHER INFORMATION: /product= "FAEI from Arabidopsis"
US-09-362-633-1

Query Match 7.5%; Score 210; DB 4; Length 1641;
Best Local Similarity 53.0%; Pred. No. 2.6e-37;
Matches 664; Conservative 0; Mismatches 435; Indels 153; Gaps

QY 1177 CACTCGGTTTCAAGAAAGAGATCTTCAACAAGCCTCAGCATAGGCGACGACATACGTC 1236
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QY 1237 CAAGATTCATCTCTTCATCAGAAAACATPACACAGATGAAGAGGTGCTGAAGAGCCT 1296
Db 425 CTGAGGAGCACTATTCACGTACACCGCGGAGAGACTTTTGACACGCTCAGGTGAAGAGACAG 484
QY 1297 CTACAGTCAATCTTTGGACACCTAGACGCAACTTTGGAGAAAGCAGACAGTGTAAAACTTAAG 1356
Db 485 AGAAGGTTATCATCGTGCGCTCGAAATTCATTGTGAGAAACCAAGATTAACTTAACTTACG 544

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2	1162	41.8	1653	9	US-09-938-842A-2597	Sequence 2597, Ap
3	1157.4	41.6	1650	10	US-09-883-797-7	Sequence 7, Appl1
4	792	28.5	811	10	US-09-770-445-774	Sequence 774, Appl
c	283.2	10.2	1548	10	US-09-883-797-13	Sequence 13, Appl
5	283.2	10.2	1548	10	US-09-883-797-13	Sequence 13, Appl
6	278	10.0	1587	9	US-09-938-842A-1598	Sequence 1598, Ap
7	273.8	9.8	1530	9	US-09-938-842A-1205	Sequence 1205, Ap
8	269	9.7	1560	10	US-09-883-797-1	Sequence 1, Appl1
9	269	9.7	1563	9	US-09-938-842A-1552	Sequence 1552, Ap
10	268.4	9.6	1611	10	US-09-883-797-9	Sequence 9, Appl1
11	249.6	9.0	409	10	US-09-878-574-4051	Sequence 4051, Appl
12	249	9.0	1502	10	US-09-883-797-11	Sequence 11, Appl
13	247.4	8.9	1491	10	US-09-892-325-5	Sequence 3, Appl1
14	247.4	8.9	1494	9	US-09-938-842A-569	Sequence 569, Appl
15	247.4	8.9	1807	10	US-09-892-325-2	Sequence 2, Appl1
16	247.4	8.9	3722	10	US-09-892-325-1	Sequence 1, Appl1
17	238.8	8.6	1736	10	US-09-877-476-5	Sequence 5, Appl1
18	229.6	8.3	1521	10	US-09-877-476-39	Sequence 39, Appl
19	228.8	8.2	1521	10	US-09-877-476-21	Sequence 21, Appl

20	228	8.2	1521	10	US-09-877-476-32	Sequence 25, Appl
21	228	8.2	1521	10	US-09-877-476-35	Sequence 37, Appl
22	227.6	8.2	1518	10	US-09-877-476-17	Sequence 17, Appl
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24	227.6	8.2	1521	10	US-09-877-476-33	Sequence 13, Appl
25	227.2	8.2	1524	10	US-09-877-476-23	Sequence 23, Appl
26	226.4	8.1	1521	10	US-09-877-476-9	Sequence 9, Appl
27	226.4	8.1	1521	10	US-09-877-476-11	Sequence 11, Appl
28	226	8.1	1521	10	US-09-877-476-3	Sequence 7, Appl
29	226	8.1	1521	10	US-09-877-476-7	Sequence 41, Appl
30	225.6	8.1	1521	10	US-09-877-476-31	Sequence 31, Appl
31	222.8	8.0	1521	10	US-09-877-476-3	Sequence 41, Appl
32	221.2	8.0	1521	10	US-09-877-476-29	Sequence 29, Appl
33	213.2	7.7	1521	10	US-09-877-476-1	Sequence 1, Appl
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36	206.4	7.4	1521	10	US-09-883-797-5	Sequence 5, Appl
37	206.2	7.4	1512	10	US-09-883-797-3	Sequence 3, Appl
38	189.2	6.8	387	10	US-09-878-574-1.1065	Sequence 1065, Appl
39	177.4	6.4	2000	9	US-09-938-8424-5275	Sequence 5275, Ap
40	175	6.3	343	10	US-09-938-8424-2604	Sequence 2604, Appl
41	173.6	6.2	468	10	US-09-938-8424-253	Sequence 253, Appl
42	137.8	5.0	1431	9	US-09-938-8424-1967	Sequence 1967, Ap
43	134.6	4.8	276	10	US-09-878-574-12488	Sequence 12488, Ap
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RESULT 1
US-09-905-657-1
; Sequence 1, Application US/09905657
; Patent No. US20020038471A1
; GENERAL INFORMATION:
; APPLICANT: BAYER AG
; TITLE OF INVENTION: Use of VEGFAE for Identifying
; TITLE OF INVENTION: active compounds
; FILE REFERENCE: Le A 34 730
; CURRENT APPLICATION NUMBERS: US/09/905,657
; CURRENT FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2782
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
FEATURE:
; NAME/KEY: CDS
; LOCATION: (176)..(583)
; NAME/KEY: CDS
; LOCATION: (1119)..(1745)
; NAME/KEY: CDS
; LOCATION: (1821)..(2438)
US-09-905-657-1

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Query Match	100.0%	Score 2782;	DB 10;	Length 2782;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2782; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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241 CGGTCTTAACGGCGGCTCCCAACGTTCTCGGTTAGGTCAGAGACGTTTGGCTGATT 300
241 CGGTCTTAACGGCGGCTCCCAACGTTCTCGGTTAGGTCAGAGACGTTTGGCTGATT 300
301 TCTTCAGTCGTGAATCTGAATAGCTGAATCTGGTTACCACTACCTATTAACCATGC 360
301 TCTTCAGTCGTGAATCTGAATAGCTGAATCTGGTTACCACTACCTATTAACCATGC 360
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541 TCTTATGATTTGCTGTTTACAGCCCTCGATGACCAAGATACGTTCCCACTTTTC 600
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1861 TGAAGATTAAGTACGACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
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Db	2521	ATTACTGATCATTCGATATCAAGTCTGTTATAGAAATGATGTGGCTAGAGTCCGTTC	2580
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Qy	2641	TTAAGAAAAAAACTCTCTCTAGTTGATAGAACGATGGCATCTGTAATTCCTTAAT	2700
Db	2641	TTAAGAAAAAAACTCTCTCTAGTTGATAGAACGATGGCATCTGTAATTCCTTAAT	2700
Qy	2701	ATGTCAAGTAAACAATTTCTTTTTAAGCAATCTAATATTCAGATACATATAAATTA	2750
Db	2701	ATGTCAAGTAAACAATTTCTTTTTAAGCAATCTAATATTCAGATACATATAAATTA	2750
Qy	2761	GTTTACGCTGATATAAGAAAGATC 2782	
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RESULT 2

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? Sequence 2597, Application US/09938842A
? Patent No. US20020160378A1
?
? GENERAL INFORMATION:
? APPLICANT: Harper, Jeff
? APPLICANT: Kieps, Joel
? APPLICANT: Wang, Xun
? APPLICANT: Zhu, Tong
?
? TITLE OF INVENTION: STRESS-REGULATED GENES OF
? TITLE OF INVENTION: SAME, AND METHODS OF USE
? FILE REFERENCE: SRIPI300-3
?
? CURRENT APPLICATION NUMBER: US/09/938, 842A
?
? CURRENT FILING DATE: 2001-08-24
?
? PRIOR APPLICATION NUMBER: US 60/227, 866
?
? PRIOR FILING DATE: 2000-08-24
?
? PRIOR APPLICATION NUMBER: US 60/264, 647
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? PRIOR FILING DATE: 2001-01-16
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? PRIOR FILING DATE: 2001-06-22
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? NUMBER OF SEQ ID NOS: 5379
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Query Match	41.8%;	Score 1162;	DB 9;	Length 1653;
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Matches 1247;	Conservative	0;	Mismatches	0;
			Indels	75;
			Gaps	11;

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Db	407	AGGTGACAAAAGAAAGGTTTCATGAACTAGCGAGAAATAATCAGGAAAGTTCCACGAAAGGA	466
QY	1177	CACGCGGTTCAAGAGAGATCTTTCACGCGTCCAGGCATAGCGACAGAGATACGCTTC	1236
Db	467	CACTCGGTTTCAAGAAAGAGATCTTTCACAGGCTCCAGGCATAGCGACAGAGATACGCTTC	526
QY	1237	CAGATCCATCTCTTCATCAGAAAACATTAACAACGATGAAAGAGAGTGTGTGAAGAAGCT	1296
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QY	1297	CTACAGGATCCTTTGGAGCAGCTAGAGAACTCTTTCAGAAAGAACAGGTGTAACCTAAG	1356
Db	587	CTACAGGATCCTTTGGAGCAGCTAGAGAACTCTTTCAGAAAGAACAGGTGTAACCTAAG	646
QY	1357	ACGTTGGTGCCTCTGTGGTTAACTGTAGACTTTTCAACCCGACACCGTCGTTGCCGAA	1418
Db	647	ACGTTGGTGCCTCTGTGGTTAACTGTAGACTTTTCAACCCGACACCGTCGTTGCCGAA	706
QY	1417	TGCTGATTAACATTACAGATGAGAGGAACATACTTACTTAACAACCTTGGAGGATGG	1478
Db	707	TGCTGATTAACATTACAGATGAGAGGAACATACTTACTTAAACAACCTTGGAGGATGG	766
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QY	1537	ATAGCTATGCTGTTGTTGTAGAGTACTGAGATGGTTGGGTATATATTTGGTACGTGGGAAGTG	1596
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QY	1597	ACAAGTAAATGCTATACGTAATTTGTTCTTTAGATAGGGTGTCTGCCGTTATGCT	1655
Db	887	ACAAGTAAATGCTATACGTAATTTGTTCTTTAGATAGGGTGTCTGCCGTTATGCT	946
QY	1657	CTAACCGTCGTCGAGACTTTCGCCATGCTAATGTAACCGTCTCGAGCACAATTGTCGCAATC	1718
Db	947	CTAACCGTCGTCGAGACTTTCGCCATGCTAATGTAACCGTCTCGAGCACAATTGTCGCAATC	1006
QY	1717	ATAAGGCTGCTGACGACCGTAGCTTCAGGTTTCATTTCATTTTGGTATTATTCGTTTAC	1778
Db	1007	ATAAGGCTGCTGACGACCGTAGCTTCAGGTTTCATTTCATTTTGGTATTATTCGTTTAC	1032

[illegible]

QY 2377 AGAAGCCAAACAGAAACATCTTGGGTGATTGCATCAACCGTTACCGTGTGCTCTCT 2436
 |||||
 DB 1592 AGAAGCCAAACAGAAACATCTTGGGTGATTGCATCAACCGTTACCGTGTGCTCTCT 1651
 QY 2437 AA 2438
 ||
 DB 1652 AA 1653

RESULT 3

US-09-883-797-7
 ; Sequence 7, Application US/09883797
 ; Patent No. US2002006123A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jaworski, Jan G.
 ; APPLICANT: Post-Belienmiller, Marsha A.
 ; APPLICANT: Todd, James
 ; TITLE OF INVENTION: FATTY ACID ELONGASES
 ; FILE REFERENCE: 07148/064001
 ; CURRENT APPLICATION NUMBER: US/09/883,797
 ; CURRENT FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 08/868,373
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO: 7
 ; LENGTH: 1650
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-883-797-7

Query Match 41.6%; Score 1157.4; DB 10; Length 1650;
 Best Local Similarity 94.2%; Pred. No. 2.5e-229;
 Matches 1243; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 1117 AGGTGACAAAGAGAGTTCATAGAACTAGCGAAGAAATCAGGGAAGTTGCGAGAAAGA 1176
 |||||
 DB 407 AGGTGACAAAGAGAGTTCATAGAACTAGCGAAGAAATCAGGGAAGTTGCGAGAAAGA 466
 QY 1177 CACTGCGTTCAAGAGAGATCTTCAAGCCGACGCAATAGGCGAGACATACGTCC 1236
 |||||
 DB 467 CACTGCGTTCAAGAGAGATCTTCAAGCCGACGCAATAGGCGAGACATACGTCC 526
 QY 1237 CAAGATCCATCTCTTCATCAGAAACATCAACAGATGAAGAAGTCTGTAAGAGCTT 1296
 |||||
 DB 527 CAAGATCCATCTCTTCATCAGAAACATCAACAGATGAAGAAGTCTGTAAGAGCTT 586
 QY 1297 CTACAGTATCTTTGGAGAGCTAGAGAACTCTTCGAGAAGACACCTGTAAGAACTTAAG 1356
 |||||
 DB 587 CTACAGTATCTTTGGAGAGCTAGAGAACTCTTCGAGAAGACACCTGTAAGAACTTAAG 646
 QY 1357 AGCTTGGTCTCTTGTGTTAGTACTGTAGCATTTTCAACCCGACACCGTGTGTCGCAA 1416
 |||||
 DB 647 AGCTTGGTCTCTTGTGTTAGTACTGTAGCATTTTCAACCCGACACCGTGTGTCGCAA 706
 QY 1417 TGGTGTAAACATTAACAAGATGAGAGGAGACATTAAGTAAACAACCTTGAGGGATGG 1476
 |||||
 DB 707 TGGTGTAAACATTAACAAGATGAGAGGAGACATTAAGTAAACAACCTTGAGGGATGG 766
 QY 1477 GATGTTGGCTGGAATCATAGCTATGATCTGCTGTGACATGCTTCACTTAACCTTA 1536
 |||||
 DB 767 GATGTTGGCTGGAATCATAGCTATGATCTGCTGTGACATGCTTCACTTAACCTTA 826
 QY 1537 ATAGTATCTGTTGTTGAGTACTGAGATGGTGGTATATTTGTTAGTGGTGGAGTGG 1596
 |||||
 DB 827 ATAGTATCTGTTGTTGAGTACTGAGATGGTGGTATATTTGTTAGTGGTGGAGTGG 886
 QY 1597 ACAAGTCAATGGTTATACCTAATGTTCTTTAGATGGGTTGTTGCGGTTATGCTT 1656
 |||||
 DB 887 ACAAGTCAATGGTTATACCTAATGTTCTTTAGATGGGTTGTTGCGGTTATGCTT 946
 QY 1657 CTAAACGTTGTTGACTTTCGCACTGTAAGTACCGTTCGAGACATTTGTCGAACCTC 1716
 |||||

DB 947 CTAAACGTTGTTGACTTTCGCACTGCTAAGTACCGTTCGAGACATTTGCCAAGCTC 1006
 |||||
 QY 1717 ATAGGCTGCTGACGACCGTAGCTAGCTTCACTTATTTGGTATTAATTCGTTTAC 1776
 |||||
 DB 1007 ATAGGCTGCTGACGACCGTAGCTTCACTTATTTGGTATTAATTCGTTTAC 1032
 QY 1777 AATCTCTTGACCGACCTAGTAACTAATTTTGTGTGTTTATAGAGTGTACACAGAG 1836
 |||||
 DB 1033 -----AGAGTGTACACAGAG 1051
 QY 1837 AAGATCAACAGAGATTCAAGGGGTTAAGATTAAGTGAACATTTATGAAAGTTGAGGTG 1896
 |||||
 DB 1052 AAGATCAACAGAGATTCAAGGGGTTAAGATTAAGTGAACATTTATGAAAGTTGAGGTG 1111
 QY 1897 AAGCTCTCAAGCAACATCACTACTAGTGGTCCCTGTTGCTTACCTTCTCGACAGC 1956
 |||||
 DB 1112 AAGCTCTCAAGCAACATCACTACTAGTGGTCCCTGTTGCTTACCTTCTCGACAGC 1171
 QY 1957 TTCTCTTCTTGTGCTGCTTGTCTCCGCAACATTTCTACCTGCTGCAAAAGCTCCAA 2016
 |||||
 DB 1172 TTCTCTTCTTGTGCTGCTTGTCTCCGCAACATTTCTACCTGCTGCAAAAGCTCCAA 1231
 QY 2017 CCAGTCTCTTCTACTTCTCCGCAACGCAAAACATGGAATCAAGTCTTCTCTCCG 2076
 |||||
 DB 1232 CCAGTCTCTTCTACTTCTCCGCAACGCAAAACATGGAATCAAGTCTTCTCTCCG 1291
 QY 2077 ATCTGTCAAGCATCATCCGAGTACAGTCCCTTCAGACATTTTGTGCTTCAGC 2136
 |||||
 DB 1292 ATCTGTCAAGCATCATCCGAGTACAGTCCCTTCAGACATTTTGTGCTTCAGC 1351
 QY 2137 CGGCAAGCAAGTAGTGTGTTGAAGAGCTTCAAAAGATCTAGGCTTGAAGAGATA 2196
 |||||
 DB 1352 CGGCAAGCAAGTAGTGTGTTGAAGAGCTTCAAAAGATCTAGGCTTGAAGAGATA 1411
 QY 2197 TGGAGCTCTTAGATGACACTTCAAGGTTTGAAGAGCTTCTAGCAATGAGTGGT 2256
 |||||
 DB 1412 TGGAGCTCTTAGATGACACTTCAAGGTTTGAAGAGCTTCTAGCAATGAGTGGT 1471
 QY 2257 ATAGTGTGCTTACATGAGAGGCAAGAAAGTTCGTGAGAGCGATAGGTTTGGCA 2316
 |||||
 DB 1472 ATAGTGTGCTTACATGAGAGGCAAGAAAGTTCGTGAGAGCGATAGGTTTGGCA 1531
 QY 2317 TCGCTTTCGTTCTGTTTAACTGTAACAGTGTGTGTAAGGCAATGAGAAAGTGA 2376
 |||||
 DB 1532 TCGCTTTCGTTCTGTTTAACTGTAACAGTGTGTGTAAGGCAATGAGAAAGTGA 1591
 QY 2377 AGAAGCCAAACAGAACATCTTGGTGGATGATCAACCGTTACCGTGTGCTCTC 2435
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 DB 1592 AGAAGCCAAACAGAACATCTTGGTGGATGATCAACCGTTACCGTGTGCTCTC 1650

RESULT 4

US-09-770-445-774/c
 ; Sequence 774, Application US/09770445
 ; Patent No. US20020023281A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goriach, Jörn
 ; APPLICANT: An, Yong-Olang
 ; APPLICANT: Raines, Jennifer L.
 ; APPLICANT: Yu, Yang
 ; APPLICANT: Rameaka, Joshua G.
 ; APPLICANT: Page, Amy
 ; APPLICANT: Matthew, Abraham V.
 ; APPLICANT: Ledford, Brooke L.
 ; APPLICANT: Woessner, Jeffrey P.
 ; APPLICANT: Haas, William David
 ; APPLICANT: Garcia, Carlos A.
 ; APPLICANT: Kriker, Maja
 ; APPLICANT: Slader, Ted
 ; APPLICANT: Davis, Keith R.
 ; APPLICANT: Allen, Keith

APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 20305 (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIORITY FILING DATE: 2000-01-27
PRIORITY FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 774
LENGTH: 811
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1)...(811)
OTHER INFORMATION: n = A,T,C or G
US-09-770-445-774

Query Match 28.5% Score 792; DB 10; Length 811;
Best Local Similarity 99.0% Pred. No. 5,4e-154;
Matches 792; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

1865 GATAGTAGAGACTTAATGGAAGTTGGAGTGAAGCTCTCAAGCAAAACATCACTACTT 1924
1865 GATAGTAGAGACTTAATGGAAGTTGGAGTGAAGCTCTCAAGCAAAACATCACTACTT 1924
800 GATAGTAGAGACTTAATGGAAGTTGGAGTGAAGCTCTCAAGCAAAACATCACTACTT 741
1925 AGGTCT 1984
1925 AGGTCT 1984
740 AGGTCT 681
1985 AACCTTCTCACT 2044
1985 AACCTTCTCACT 2044
680 AACCTTCTCACT 621
2045 AAAAACAATGGAATCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2104
620 AAAAACAATGGAATCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 561
2105 CAAGCTGCT 2164
560 CAAGCTGCT 501
2165 TCAAAAGAACTAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2224
500 NCAAAAGAACTAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 441
2225 GTTGAAGAACTCTAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2284
440 GTTGAAGAACTCTAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 381
2285 AAGTCTCTAGAGGCAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2344
380 AAGTCTCTAGAGGCAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 321
2345 CAGTCTCTAGAGGCAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2404
320 CAGTCTCTAGAGGCAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 261
2405 GGATGATCAACCGTCTAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2464
260 GGATGATCAACCGTCTAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 201
2465 GTAAGATCTCTAATTAATCAACCAAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2524
200 GTAAGATCTCTAATTAATCAACCAAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 141
2525 ACTATCT 2584
140 ACTATCT 81

2585 TCAACTGTTTATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTAA 2644
80 TCAACTGTTTATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTAA 21
2645 AGAAAAAACTCTCTTTAG 2664
20 AGAAAAAACTCTCTTTAG 1

RESULT 5

US-09-883-797-13
Sequence 13, Application US/09883797
Patent No. US20020066123A1

GENERAL INFORMATION:

APPLICANT: Jaworski, Jan G.
APPLICANT: Post-Bellemiller, Martha A.
TITLE OF INVENTION: FATY ACID ELONGASES
FILE REFERENCE: 07148/064001
CURRENT APPLICATION NUMBER: US/09/883,797
CURRENT FILING DATE: 2001-06-18
PRIORITY FILING DATE: 08/868,373
PRIORITY FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13

LENGTH: 1548
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-883-797-13

Query Match

Best Local Similarity 10.2% Score 283.2; DB 10; Length 1548;
Matches 723; Conservative 0; Mismatches 423; Indels 156; Gaps 3;

1133 GTTATAGAACTAGGAGAAATCAAGGAGTTCGACGAGAGACACTCGGTTTCAGAA 1192
396 GTTATAGAACTAGGAGAAATCAAGGAGTTCGACGAGAGACACTCGGTTTCAGAA 455
1193 GAGATCTTACAGCTTACGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 1252
456 CAAGATCTTACAGCTTACGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 515
1253 ATCAGAAACATTAACAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 1312
516 GTTTCACACGAGATTTACATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 575
1313 AGCACTAGACGAGATTTACATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 1372
576 GTTTCACACGAGATTTACATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 635
1373 GGTATCTAGGATTTACATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 1432
636 GTTATCTAGGATTTACATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 695
1433 CAAGATGAGGAGAACTAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 1492
696 TAACTTGAAGTAACTAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 755
1493 CATAGCTATGATCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1552
756 TATGCTGATGATCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 815
1553 TGTGATCTGATGATCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1612
816 TGTGATCTGATGATCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 875
1613 AACTAATGATCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1672
876 ACCGAACTGATCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 935
1673 CTTCGCACTGATCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1732

US-09-883-797-1
 : Sequence 1, Application US/09883797
 : Patent No. US2002006123A1
 : GENERAL INFORMATION:
 : APPLICANT: Jaworski, Jan G.
 : APPLICANT: Post-Beltlemiller, Martha A.
 : APPLICANT: Todd, James
 : TITLE OF INVENTION: FATTY ACID ELONGASES
 : FILE REFERENCE: 07148/064001
 : CURRENT APPLICATION NUMBER: US/09/883,797
 : CURRENT FILING DATE: 2001-06-18
 : PRIOR APPLICATION NUMBER: 08/868,373
 : PRIOR FILING DATE: 1997-06-03
 : NUMBER OF SEQ ID NOS: 22
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 1
 : LENGTH: 1560
 : TYPE: DNA
 : ORGANISM: Arabidopsis thaliana
 US-09-883-797-1

Query Match 9.7%; Score 269; DB 10; Length 1560;
 Best Local Similarity 55.2%; Pred. No. 8.4e-46;
 Matches 723; Conservative 0; Mismatches 430; Indels 156; Gaps 4;

QY 1123 CAAAAGAGAGTTCTATGAACTAGCGAAGAAATCAGGAGAGTTGAGAGAGACACTCG 1182
 DB 392 CAGTAGATGCTCTTACGATGACGAAATGATCTTACCGATGACAGGTTTC 451
 QY 1183 GTTTCAGAGAGATCTTACAGCCCTCAGGATAGCGAGACATACCTCCCAAGT 1242
 DB 452 AGTTCGCGAAGAGATTCGAAACCGGCGTTGGAGAGACATATCTGCGACGTG 511
 QY 1243 CCATCTTCATCAGAAACATATACAGATGAGAGAGTGGAGAGAGCTCTACAG 1302
 DB 512 GCATTAATTCAGCCCGCCGAGAGCTAATATGTGAGAGCGACGCGGAGAGCTGAACCG 571
 QY 1303 TGATCTTGGAGACATGAGACAGACTCTCGAAGAGACAGTGAACCTTAAGAGCTTG 1362
 DB 572 TTATGTTGAGAGCTTATGATCCCTCTCGAAGAAACCGGAAATTAACCGCGGAGAGCG 631
 QY 1363 GTGCTGTTGGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1422
 DB 632 GAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
 QY 1423 TAAACATTAACAGATGAGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTA 1482
 DB 692 TGAACCATTAACAGATGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAAT 751
 QY 1483 CGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1542
 DB 752 CCGCGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 811
 QY 1543 ATGCTGTTGGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1602
 DB 812 ACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 871
 QY 1603 CAATGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1662
 DB 872 CAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 931
 QY 1663 GTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1722
 DB 932 GCGCTCAAGACCGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 991
 QY 1723 CTGCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1782
 DB 992 GATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1015
 QY 1783 TTGACGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1842
 DB 1016 -----GCGTGTACAGAGAGAGAGAG 1036

QY 1843 AACAGATTCAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1902
 DB 1037 AGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1096
 QY 1903 TCAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1962
 DB 1097 TGAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1156
 QY 1963 TCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2022
 DB 1157 TCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1173
 QY 2023 CTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2082
 DB 1174 -----AAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 QY 2083 CCAAGCATATCCCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2142
 DB 1201 --AAACGATATATCCCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1258
 QY 2143 GCAAGTAGATGCTTGAAGAGCTTCAAAAGATCTAGGCTTGAAGAGATGATGATGATGATGAT 2202
 DB 1259 GTAGAGGAGTCTAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1318
 QY 2203 CTTTGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2262
 DB 1319 CTTTGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1378
 QY 2263 TGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2322
 DB 1379 TGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1438
 QY 2323 TCGCTTGTGTTTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2379
 DB 1439 TTGATGAGGTTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1498
 QY 2380 AGCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2428
 DB 1499 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1547

RESULT 9

US-09-938-842A-1552
 : Sequence 1552, Application US/09938842A
 : Patent No. US20020160378A1
 : GENERAL INFORMATION:
 : APPLICANT: Harper, Jeff
 : APPLICANT: Kreps, Joel
 : APPLICANT: Wang, Xun
 : APPLICANT: Zhu, Tong
 : TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 : FILE REFERENCE: SCRI1300-3
 : CURRENT APPLICATION NUMBER: US/09/938,842A
 : CURRENT FILING DATE: 2001-08-24
 : PRIOR APPLICATION NUMBER: US 60/227,866
 : PRIOR FILING DATE: 2000-08-24
 : PRIOR APPLICATION NUMBER: US 60/264,647
 : PRIOR FILING DATE: 2001-01-16
 : PRIOR APPLICATION NUMBER: US 60/300,111
 : PRIOR FILING DATE: 2001-06-22
 : NUMBER OF SEQ ID NOS: 5379
 : SEQ ID NO 1552
 : LENGTH: 1563
 : TYPE: DNA
 : ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1552

Query Match 9.7%; Score 269; DB 9; Length 1563;
 Best Local Similarity 55.2%; Pred. No. 8.4e-46;
 Matches 723; Conservative 0; Mismatches 430; Indels 156; Gaps 4;
 QY 1123 CAAAAGAGAGTTCTATGAACTAGCGAAGAAATCAGGAGAGTTGAGAGAGACACTCG 1182


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Db 392 CAGTAGATCGTTTGAAGATGAGGAAATGGATCATTCACCGATGACGGTTC 451
Oy 1183 GTTCAAGAGAGATCTTACAGCCTAGGCATAGGCGACAGACATAGCTCCAAAT 1242
Db 452 AGTTCAGCAAGATCTGCAACGGCGGCTTGGAGACGACGATCTGCCACGTG 511
Oy 1243 CCATCTTTCATCAAAAACATTAACAGATGAAGAGGTGTGAAGAGCTCTACAG 1302
Db 512 GCATTAATCAAGCGCCCGAAGCTTAATATGTCAAGGACAGCTGCCAAGCTGAAGCG 571
Oy 1303 TGAATCTTGGACACTAGCAAGACTCTTCAGAGACAGAGCTGAACCTTAAGAGCTG 1362
Db 572 TTAATGTTGGACCTTAATTCCTCTTGAGAAAAACCGGATTAACCGGCGGAAGTGG 631
Oy 1363 GTGCTCTGTGTGTAAGTGAAGTTCACCCGACACCGCTGCTGCCAATGTGA 1422
Db 632 GAATCTTGAATGAATCAACGCTTATTCATCCGACCGCTCTATAGCGATGATCG 691
Oy 1423 TAAACATTAACAGAGAGGAGGAACTTAATTAACAACTTGAGGAGGATGTT 1482
Db 692 TGAACATTAACAGAGAGGAGGAACTTAACAACTTGAGGAGGATGTT 751
Oy 1483 CGGCTGAATCATACCTATTTGCTTGTCTGACATGCTTCAAGTCAACCTTAATAGT 1542
Db 752 CGCGGAGATTAATCTCANTGATCTGCTAACAATCTCTCAAGAAACCTTAATCTT 811
Oy 1543 ATGCTGTGTGTGTAAGTGAAGTGAAGTGGTGAATGTTGTAAGTGAAGTGAAGT 1602
Db 812 AGCGTGTGTGTGTAAGTGAAGTGAAGTGGTGAATGTTGTAAGTGAAGTGAAGT 871
Oy 1603 CAATGTTATACCTAATGTTCTTAGAGTGGTGTCTCCGTTAGCTCTCAAC 1662
Db 872 CAATGTTCTCTGCACTGATGATCTTCGATGGGAGCTGATGCTCTCTCAAC 931
Oy 1663 GTGCTGTGACTTTCGCCATGCTAGTACCTGCGAGCATTGTCGAATCTAAG 1722
Db 932 GCGGCAAGACCGGAGAAAGTCAAAAGTACTGCTGTCAGCTGTCGAACATCAAAAG 991
Oy 1723 CTGCTGACGACCGTACCTTACGCTTCAATTTGTTAATTCGTTTCAATCTC 1782
Db 992 GATCAGACGACAAAGATCAATTT----- 1015
Oy 1783 TTGACCGACCTGTAATATTTGTGTGTTTGAAGTGTGACGAGAAAGATG 1842
Db 1016 -----GCGTGAACGAGAAAGACG 1036
Oy 1843 AACAGATTCAGAGGTTGAAGATAGAGACTTAATGAAGTGGAGTGAAGCTC 1902
Db 1037 AGAGAGAAACATGCTGTCTTTAGCTAGAGAGCTATGCTGTGCGCGAGAGAGCTC 1096
Oy 1903 TCAACACAAACATCACTACCTTAGCTCTGTGCTTCTTCTCCGACAGCTTCTCT 1962
Db 1097 TGAACAAACAACTCAAGCTTAGAGACGATGTTCTTCATGTTCAAGAGAGTGTATGT 1156
Oy 1963 TCTTGTGCTGTGCTGCGCGGACATCTCACTGCTGCCAAAGCTCACACACTT 2022
Db 1157 TCTTATTTCTTGTGCT----- 1173
Oy 2023 CCTTCTACTTCCGCAACCGCAAAACCAATGATCAAGTCTTCTCTCCGATCTGT 2082
Db 1174 -----AAAGAGATGTTCAAGTTAAAGTT----- 1200
Oy 2083 CCAAGCATACATCCCGGACTCAAGCTGCTTGGAGCATTTTGTCTTCAACGGCGCA 2142
Db 1201 --AAACCGATATTCCTCGGATTTCAAGCTGTTGAGCATTTCTGATTCACGCGAG 1258
Oy 2143 GCAAGTGTGCTTGAAGGCTTCAAAAGATTCAGCTGAGTGAAGAGATATGAGAG 2202
Db 1239 GTAGAGCGTCTTACAGAGTGCAGAAATCTTGATCTCAAAAGTTGGCACTGGAAC 1318
Oy 2203 CTTTGAAGTGAACCTTCAAGAGTTGGAACACTTCTAGCAGTGAATCTGATAGT 2262
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Db 1319 CTTTAGAATGACTTTCACAGATTTGTAACTTTCAGATGACCTGCTTGGTATAGA 1378
Oy 2263 TGGCTTACATGAGGCAAGAAAGTGTCTGAGAGCCATAGGCTTGGCAGATGCTT 2322
Db 1379 TGGCTTATACCAAGGTAAGGCTGAGTAAAGCTGTGACCGCACTTGTGCAGATTCGT 1438
Oy 2323 TCGGCTGCTGTTTAACTTAACAGAGTGTGTGGAAGCAATGAGAGAGT---GAGA 2379
Db 1439 TTGATCGGCTTCAAGTGTAAATAGTCGGCTTTGGAAGCGTTACGACCGGTTTCACGG 1498
Oy 2380 AGCCAACCAAGAAACATTCCTGGGTGATTCATCAACCGTTACCTGT 2428
Db 1499 AGAGATGACCGGATATGCTTGGCGTGTTCATGATCAATATCCGT 1547

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```

RESULT 10
US-09-883-797-9
; Sequence 9, Application US/09883797
; Patent No. US20020066123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Bellienmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-883-797-9

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Query Match 9.6%; Score 268.4; DB 10; Length 1611;
Best Local Similarity 54.5%; Pred. No. 1,1e-45;
Matches 722; Conservative 0; Mismatches 446; Indels 156; Gaps 3;

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Oy 1114 TTAGGTGACAAAGAGATTCATAGACTAGACGAGAAATCAGGAGATTCGACGAG 1173
Db 440 TTGAGTTAGATGACGAAAGTTATATGATCATTTAGTTGAAAGATTTCAATGAGT 499
Oy 1174 AGACACTCGGTTCAAGAAAGAGATCTTAACAGCTCAGGATAGGCGACAGACATACG 1233
Db 500 CATCTTAAAGTTTCAAGAGAAAGATTTGAACGTTCTGCTTAAAGAGAAAGACTTATC 559
Oy 1234 TCCCAAGATCCATCTTTCATCAGAAACATTAACAAGATGAAGAAAGTCCGTAAGAG 1293
Db 560 TCCCTGAACCTTACATTTATTCCTCCGAGGCGTACGATAGGCGCTCGAGAGAAAT 619
Oy 1294 CCTCTACATGATCTTGGAGCACTAGACAACTCTCGAAGACAGCTGTAAACCTA 1353
Db 620 CTGAGAGATTAATGTTGCTGCTTGAATAGCTTTTCAGAAATFACCAAGATTAACCTTA 679
Oy 1354 AAGACGTGTGCTCTTGTGTTAACTGATGATTTTCAACCGGACACCGCTGTCTCCG 1413
Db 680 GGAATATGTGTGCTGTTGTTGAATTTGATGCTTGAATCTTCAACCTTCGTTGTCAAG 739
Oy 1414 CAATGTTATTAACATTAACAGATGAAGGAGAACTACTTACTTCAACCTTGAGGGA 1473
Db 740 CTATGATTTTAAACAAGTAAAGCTTAAAGGAGAAATTTAAAGCTTTTAACTGTTGAA 799
Oy 1474 TGGAGATTCGCGTGAACATAGATTAATGATCTCTGTCGATGCTTCAAGTCAAC 1533
Db 800 TGGGCTGATGCTGCTGTTATCTATGATTAATGATTAAGTAAAGTATGTTGCAAGTTCA 859
Oy 1534 CTAAATGATGCTGTTGTTGAGTACTGAGATGCTGGGATTAATTTGATGAGTGGGA 1593
Db 860 GGAATACTATGCTGTTGTTGTTAGTACGAGAACTTACTCAGAAATGTTATTTGGGA 919

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Db 448 ATTCCCTCCACACCAACCATGGACGGCTAGAACGAGCTCAGATGTTATCTTCGAG 507
 Oy 1314 GCACCTAGCAGACTCTTGAGAGACAGCTGTAACCTAAGACGTTGTCCTGTG 1373
 Db 508 GCCATGGACGATCTTTTCAAGAAACCGCTTAAAGCTAAAGAGCTGACATCTTATC 567
 Oy 1374 GTTACCTGATCTTTCACCCGACCGTGTGCGGAATGAGTAAACATATAC 1433
 Db 568 GTCACTGCTCTCTTTTCTCCACACCATGCTCTCAGCTATGCTATCAACAAATAT 627
 Oy 1434 AAGATGAGAGGAAACATTAAGTTACAACTTGAGGAGATGAGATGTTGCGTGAATC 1493
 Db 628 AAGCTTAGAGATTAATACAGAGCTTCAATTTTCGGGATGAGGCTGACGGCGCTG 687
 Oy 1494 ATACCTATGATCTTCTGCTGACATGCTTACGTTAACTTAATAGTTATGCTGTG 1553
 Db 688 ATCTAGTGTATCAGCCCGGAGCTGCTCCAAAGTTATCCCAATTCAAATGACATATC 747
 Oy 1554 GTGAGTACTGATGTTGGGTATATGTTACGTGACGTGGAAGTGAACATGATGTTATA 1613
 Db 748 GTCAACGAGGATCATACCCCTAATTAATCAAGGCAACGAGAGACCATGTTGTTA 807
 Oy 1614 CTTAATGTTCTTTAGAGATGGTGTTCCTGCTTATGCTCTTAACCTGTCGTGAC 1673
 Db 808 CCCAATGTCTCTCCGATGGTGGGACGACCATACATGTCAAACCGCGCTGAC 867
 Oy 1674 TTTGCCATGCTAATGACCTGCTGAGACATTTGCCAATCAATTAAGCTGCTGACAC 1733
 Db 868 CGGTGGGAGCAATACAACTTTCCACCTGCTCGGACACACCGGTGGGCTGACAC 927
 Oy 1734 CGTAGTTCAGGTTTCATTTTGGTATTAATTCGTTTACAACTCTTGACCGACT 1793
 Db 928 ----- 927
 Oy 1794 AGTAACTAATTTGTGTTTATAGAGTGTACAGAGAGAGATGAACAAGATTC 1853
 Db 928 -----AAGTCTTCTAGTGTCTACGACAGAGAGAGAGAGAGAGAGAC 972
 Oy 1854 AAGGGTGAAGATTAAGTGAAGCTTAATGGAAGTGAAGTGAAGCTCTCAAGACAAC 1913
 Db 973 GTTGGATCAACTTGTCCAAAGATCATGCGCATGCGCGGTGAAGCCCTCAAGCAAC 1032
 Oy 1914 ATCACTACTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1973
 Db 1033 ATCAACCATATAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1092
 Oy 1974 TTGCTCGCGGACATTTCTGACCTGCTGCAAAAACGTCACAACTCTCTCTACT 2033
 Db 1093 CTAATCGACGTAAAT----- 1109
 Oy 2034 TCCGCCACCCCAAAACCATGATGATCAAGTCTTCTCTCCATCTGTCACACCATAC 2093
 Db 1110 -----CTTCAACCCGAATGGAACCATAC 1134
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 Db 1135 ATACCGATTTCAAGCTGCGCTTGCACACTTTTGCATTCACGAGAGAGAGCGGTG 1194
 Oy 2154 CTTGAAGAGCTTCAAAAGATCTAGGCTTGAAGAGATATGAGAGCTTCTAGAGAT 2213
 Db 1195 ATGAGAGAGCTCAAAAGATCTACACTATACAGAGACACGTTGAGGCTCAAGATG 1254
 Oy 2214 ACACCTCACAGTTTGAAGACCTTCTAGAGAGGATGAGATCTGATGAGTTGCTTACATG 2273
 Db 1255 ACCTCATCTGTTTGTGAACAGCTATCTTCACTGTTATGATGACGCTTAGCTATATC 1314
 Oy 2274 GAGGCAAGGAAGTGTCTAGAGGAGATAGGTTTGGAGATCGCTTCTGCTGCTGCT 2333
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 Oy 2334 TTTAAGTGAAGAGTGTGTTGAAGGCAATGAGAGAGTGAAGAGCAACAGAGAC 2393
 Db 1375 TTCAAGTGAATCTGCGCGGTGGAATATGAACCGTATCAATTAAGA---CACCTAAGGAC 1431

Oy 2394 AATCCTGGGTGATGATCAACCGTTACCTGT 2428
 Db 1432 GGACCATGTGTCGATGTATGACCGCTTACCTGT 1466
 RESULT 14
 US-09-938-842A-569
 : Sequence 569, Application US/0993842A
 : Patent No. US20020160378A1
 : GENERAL INFORMATION:
 : APPLICANT: Harper, Jeff
 : APPLICANT: Kreps, Joel
 : APPLICANT: Many, Xun
 : APPLICANT: Zhu, Tong
 : TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 : FILE REFERENCE: SCRI300-3
 : CURRENT APPLICATION NUMBER: US/09/938, 842A
 : PRIOR FILING DATE: 2001-08-24
 : PRIOR APPLICATION NUMBER: US 60/227, 866
 : PRIOR FILING DATE: 2000-08-24
 : PRIOR APPLICATION NUMBER: US 60/264, 647
 : PRIOR FILING DATE: 2001-01-16
 : PRIOR APPLICATION NUMBER: US 60/300, 111
 : NUMBER OF SEQ ID NOS: 5379
 : SEQ ID NO 569
 : LENGTH: 1494
 : TYPE: DNA
 : ORGANISM: Arabidopsis thaliana
 US-09-938-842A-569
 Query Match 8.9%; Score 247.4; DB 9; Length 1494;
 Best Local Similarity 53.9%; Pred. No. 2.4e-41;
 Matches 698; Conservative 0; Mismatches 441; Indels 156; Gaps 3;
 Oy 1134 TTCAATAGACTAGCGAGAAATCAGGAGTTGACGAGAGACATCGTTTCAAGAG 1193
 Db 328 TTCAATAGACTAGCGAGAAATCAGGAGTTGACGAGAGACATCGTTTCAAGAG 387
 Oy 1194 AGGATCTTCAAGCTCAGGATAGGAGAGAGACATACGTTCCCAAGATCTCTTCA 1253
 Db 388 AGGATCTTCAAGCTCAGGATAGGAGAGAGACATCTCTCTCCCGCTATTCATTAT 447
 Oy 1254 TCAGAAAACATACAGATTAAGAGAGTGTGTAAGAGGCTCTACAGTATTTGA 1313
 Db 448 ATTCCCTCCACACCAACCATGAGCGGCTAGAACGAGGCTCAGATGTTATCTTCGAG 507
 Oy 1314 GCACCTAGCAGACTCTTGAGAGACAGCTGTAACCTAAGACGTTGTCCTGTG 1373
 Db 508 GCCATGGACGATCTTTTCAAGAAACCGCTTAAAGCTAAAGAGCTGACATCTTATC 567
 Oy 1374 GTTACCTGATCTTTCACCCGACCGTGTGCGGAATGAGTAAACATATAC 1433
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 Db 628 AAGCTTAGAGATTAATACAGAGCTTCAATTTTCGGGATGAGGCTGACGGCGCTG 687
 Oy 1494 ATACCTATGATCTTCTGCTGACATGCTTACGTTAACTTAATAGTTATGCTGTG 1553
 Db 688 ATCTAGTGTATCAGCCCGGAGCTGCTCCAAAGTTATCCCAATTCAAATGACATATC 747
 Oy 1554 GTGAGTACTGATGTTGGGTATATGTTACGTGACGTGGAAGTGAACATGATGTTATA 1613
 Db 748 GTCAACGAGGATCATACCCCTAATTAATCAAGGCAACGAGAGACCATGTTGTTA 807
 Oy 1614 CTTAATGTTCTTTAGAGATGGTGTTCCTGCTTATGCTCTTAACCTGTCGTGAC 1673
 Db 808 CCCAATGTCTCTCCGATGGTGGGACGACCATACATGTCAAACCGCGCTGAC 867

1674 TTTCGCATGCTAAGTACGCTGAGACATTTGCGAATCATATAGGCTGAGAC 1733
 868 CGGTGGGAGACCAATATCAAGCTTTCCACCTGCTCGACACCGCTGGCGTACGAC 927
 1734 CGTAGCTTCAAGTTTCATTCATTTTGGTATTAATTCGTTTACAACTTGAACCGACT 1793
 928 ----- 927
 1794 ACTAATAATTTGTGTGTTTATAGAGTGTACAGAGAGAGATGAACAAGATTC 1853
 928 -----AAGCTTTCTACTGTCTACGACAGAGAGAGAGAGAGAGAC 972
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 973 GTTGGCATCACTTGTCCAAAGATCTCATGCGCATCGCGGTGAGCGCTCAAGGCAAC 1032
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 1033 ATCAGCAGATAGTCTCTTGTCTCACTTTCGAGAGAGCTTCTCTTCTTGTCT 1092
 1974 TTGCTCGCGGAGATTTCTACCTGCTGCGCAAAAGCTCAACCACTTCTCTTCT 2033
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 2034 TCCGCCACGCAAAACCAATGATCAATGATCTTCTCTTCTCTTCTTCTCAAGCCATC 2093
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 RESULT 15
 US-09-892-325-2
 : Sequence 2, Application US/09892325
 : Patent No. US20020116735A1
 : GENERAL INFORMATION:
 : APPLICANT: Kunst et al.
 : TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
 : Involved In Very Long Chain Fatty Acid Synthesis
 : NUMBER OF SEQUENCES: 12
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Klarquist Sparkman Campbell
 : Leigh & Whinston, LLP
 : STREET: One World Trade Center, Suite
 : 1600, 121 S.W. Salmon Street
 : CITY: Portland
 : STATE: OR
 : COUNTRY: USA
 : ZIP: 97204-2988
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Disk, 3.5-inch

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows NT
 SOFTWARE: Word97 & ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/892,325
 FILING DATE: 26-Jun-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/058,947
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: David J. Earp, Ph.D.
 REGISTRATION NUMBER: 41,401
 REFERENCE/DOCKET NUMBER: 5493-50032/DJE
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (503) 226-7391
 TELEFAX: (503) 228-9446
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1807
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-892-325-2
 Query Match 8.9%; Score 247.4; DB 10; Length 1807;
 Best Local Similarity 53.9%; Pred. No. 2.6e-41;
 Matches 698; Conservative 0; Mismatches 441; Indels 156; Gaps 3;
 1134 TTCTAAGATAGGAGAAATATCGAAGAGTTCAGCAAGACATCGGTTCAAGAG 1193
 386 TTCTAAGATAGGAGAAATATCGAAGAGTTCAGCAAGACATCGGTTCAAGAG 445
 1194 AGATCTTCAAGAGCTGAGGATAGGAGAGAGATAGGATAGGATAGGATAGGAT 1253
 446 AGATCTTCAAGAGCTGAGGATAGGAGAGAGATAGGATAGGATAGGATAGGAT 505
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 1374 GTTAAGTGAAGTGTGTAACGCTTTCATGAGAGAGATGAGAGAGATGAGAG 1433
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 1434 AAGATGAGAGAGATAGGATAGGATAGGATAGGATAGGATAGGATAGGATAGG 1493
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 806 GTGAGCAGGAGATCAATAGAGAGATGATGATGATGATGATGATGATGATGAT 865
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 926 CGGTGGGAGACCAATATCAAGCTTTCCACCTGCTCGACACCGCTGGCGTACG 985
 1734 CGTAGCTTCAAGTTTCATTCATTTTGGTATTAATTCGTTTACAACTTGAAC 1793
 986 ----- 985

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DB 986 -----AAGCTTTCTACTGTGTCTACGACAGAGACAAAGAGACAC 1030
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DB 1031 GTTGGCATCACTTGTCCAAAGATCTCATGCGCATCGCGTGAAAGCCCTCAAGGCAAC 1090
OY 1914 ATCACTACCTTAGTGTGCTTGTCTTACCTTCTCCAGAGAGTCTCTCTTGTGCT 1973
DB 1091 ATCACCAATAGTGTCTTGTCTTACCGGCTCAGAACTTCTCTCTCAGCTCC 1150
OY 1974 TTGCTCCGCCGGAATCTTCACTGTGCTGCAAAAGCTCCACAACACTTCTCTACT 2033
DB 1151 CTAAATCGGACGTAAAT----- 1167
OY 2034 TCCGCCACCGCAAAACCAATGAAATCAAGCTTCTCTCCGATCTGTCCAAAGCCATAC 2093
DB 1168 -----CTCAACCCGAAATGAAACCATAC 1192
OY 2094 ATCCGGACTACAGTGTGCTTGCAGCATTTTGTCTTCCAGCGGCAAGCAAGTAGTG 2153
DB 1193 ATACGGATTTCAAGCTGTGCTTGCAGACCTTTGTGATTCACGACAGAGGACAGCGGTG 1252
OY 2154 CTTGAAGAGCTTCAAAAGATCTAGGCTTGAAGAGATATGAGAGCTTCTAGATG 2213
DB 1253 ATCGAGAGCTCCAAAGATCTACAACTATCAGAGAAACAGCTTGAAGCTCAAGATG 1312
OY 2214 ACACCTTACAGTGTGGAACCTTCTAGCAGTGCATCTGTATGAGTGTGCTTACATG 2273
DB 1313 ACACATACATCGTTTGTGTAACGCTCATCTTATGATGTAGAGCTTACATC 1372
OY 2274 GAGGCCAAGAAAGTGTGTAAGGCGATGAGGTTTGGCAGATCGCTTGGTCTGTGT 2333
DB 1373 GAGTCTAAAGGAGATGAGAGAGCGCATCGCGTTTGGCAATCGCTTTGGAGTGT 1432
OY 2334 TTTAAGTGTACAGTGTGTGTAAGGCAATGAGAGAGTGAAGAGCCAAACAGAGAAC 2393
DB 1433 TTCAGGTGTAAGTGTGCGCTGTGAAATGTAAACCGTACGATTAAAG--CACCTAAGGAC 1489
OY 2394 AATCCTTGGGTGATTTGCATCAACGTTACCTGT 2428
DB 1490 GGACCATGTGCGATTGTATGACCGTTACCTGT 1524
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Job time : 383 secs